STIC-Biotech/ChemLib

From:

Sent:

Vogel, Nancy Tuesday, April 27, 2004 1:06 PM

To: Subject:

STIC-Biotech/ChemLib sequence search 10/677,471

Please search SEQ ID NO 83 of 10/677,471 and return results to me on paper asap. Thanks,

Examiner Nancy Vogel

Art Unit 1636

Office: Remson 2A65 Mail Box: Remson 2C70

(571) 272-0780

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

'ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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Maximum Match 100%
Listing first 45 summaries
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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ALIGNMENTS

12-DEC-1997 16-DEC-1997 16-DEC-1997 16-DEC-1997 17-DEC-1997 17-DEC-1997 17-DEC-1997 18-DEC-1997 18-DEC-1997 05-JAN-1998 09-FEB-1998 03-DEC-1997; 11-DEC-1997; 11-DEC-1997; 11-DEC-1997; 01-DEC-1998; Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder. Human PRO361 protein sequence AAY17834; AAY17834 standard; protein; WO9928462-A2 Homo sapiens 12-AUG-1999 10-JUN-1999 (GETH) GENENTECH INC. (first entry) 97US-0067411P 97US-0069278P 97US-0069334P 97US-0069335P 97US-0069425P 97US-0069694P 97US-0069702P 97US-0069702P 97US-0069873P 97US-0068017P 98US-0070446P 98US-00714945P 98US-0075945P 98WO-US025108 431 A

Claim 12; Fig 37; 123pp; English. Nucleic acids encoding PRO secreted and

transmembrane proteins

Wood WI,

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Best Local
                         Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; systemic vasculitis; autoimmune-mediated renal disease; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; craft reference better disease; allergic manunological disease; transplantation associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
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99US-0123618P.
99US-0123957P.
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Ashkenazi AJ, Kabakoff RC, RC, J, Baker KP, Goddard A, , Lu Y, Pan J, Pennica Tumas D, Watanabe CK, Gurney AL, Hebo D, Shelton DL, Wood WI, Yan M; Hebert C, DL, Smith Henzel Ξ

2000-572271/53. DB; AAC58593.

Sixty four PRO polypeptides, useful in the diagnosis and treatment immune related disorders, e.g. systemic lupus erythematosis, rheumarthritis, osteoarthritis, thyroiditis and diabetes mellitus. atment of rheumatoid

Claim 33; Fig 30; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases ō, central and

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                             Modified-site
                                                                                                                                                                                                                                                           PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO241; PRO323; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
                                                                                                                                                                                                                                                                                                                                                                                           Human PRO361 polypeptide.
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48. .54
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Pred. No. 3.6e-173;
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16-DEC-1998;
22-DEC-1998;
                                                                                                                                                                                                                                                        New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP, Botstein D,
Gerritsen ME, Goddard
Hillan KJ, Kljavin IJ,
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                                                                                                                       MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ
HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                                      TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
                                                                                     EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII
                                                                         EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII
                        TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids encoding secreted as PRO polypeptides, useful as
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E, Goddard
                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative
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98US-0112850P.
98US-0113296P.
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327. .331
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A, Godowski PJ, Grimaldi CJ, Gurn
Napier MA, Roy MA, Tumas D, Woo
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                                                                                                                                                                     Score 2211; DB 3;
Pred. No. 3.6e-173;
); Mismatches 0;
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17-MAR-1999;
17-AUG-1999;
01-OCT-1999;
29-NOV-1999;
15-FEB-2000;
                  This invention relates to 59 human secreted proteins and the nucleotide sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745 represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59847-C59596. The proteins exhibit neuroprotective, dermatological, immunosuppressive, antiinflammatory, antianaemic, nootropic, antiparkinsonian,
                                                                                                                                                                                                                                                                                  Novel proteins and polypeptides useful for the treatment of e.g multiple sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
                                                                                                                                                                                                                                       Claim 114; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC disorders with as multiple sclerosis, systemic lupus erythmatosus, care also useful arthritis, and for treating myeloid or lymphoid cell codeficiencies such as anaemias by regulating haematopolesis. The proteins care also useful in compositions for bone, cartilage, tendon, ligament code are also useful in compositions for bone, cartilage, tendon, ligament code and/or nerve tissue growth or regeneration, for wound healing, tissue crepair and replacement and in the treatment of wounds, incisions and code uncers. Other uses include in the treatment of wounds, incisions and corrows system and neuropathies such as Alzheimer's and Parkinson's codiseases and Shy-Drager syndrome, and mechanical and traumatic disorders, lose used as a contraceptive, and for treating coagulation disorders such as spinal cord disorders, head trauma and stroke. The proteins may come as second as a contraceptive, and for treating coagulation disorders such as haemophilias. The protein and nuclectide sequences with cadherin codinctity are useful for treating cancer other uses for the protein conscituty are useful for treating cancer other uses for the protein codinctity are useful for treating cancer other uses for the protein codinctity are useful for treating cancer other uses for the protein codinctity are useful for treating cancer other uses for the protein codinctity are useful for treating cancer other uses for the protein of codinctity are useful for treating cancer other uses for the protein codinction of codinctity are useful for treating cancer other uses for the protein of codinction of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial, virucide, and fungicide activity. The proteins and
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                                                                                   EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
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                                                           EASPGSSSQGS1
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Human protein

sequence SEQ

ID NO:17950.

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complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotide; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 1'-end sequence, where the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CDNAs easily without any specialised methods. AAH03166 to AAH13628 and represent human amino acid sequences; and AAH13639 to AAH13632 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999; YYUF C. 27-AUG-1999; 99JP-00300253. ( 11-JAN-2000; 2000JP-00118776. 202-MAY-2000; 2000JP-00183767. 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 431; Conserv
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Ishii !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes primer sets for synlength cDNAs defined in the specification. Where a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 431 AA;
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                             TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
  TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2211; DB 4; ilarity 100.0%; Pred. No. 3.6e-173; Conservative 0; Mismatches 0;
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T, Wakama
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A, Nagai K,
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C, Otsuki
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,

DL;

Godowski PJ; Paoni NF;

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                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted and transmembrane
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 26-MAR-2003
                                ABU55934;
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Pred. No. 3.6e-173;
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22-MAY-2000
28-JUL-2000
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25-MAY-2001
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01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRO; secreted protein; transmembrane protein; anti-HTV; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; cardiant; AIDS; acquired immunodeficiency syndrome; cancer; atherosclerosis; inflammatory disease; diabetic complication;
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01-DEC-1999;
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99WO-US038301.
99WO-US030095.
2000WO-US003565.
2000WO-US004414.
2000WO-US00843.
2000WO-US00849.
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2000WO-US014042.
2000WO-US0326710.
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Baker KP, Gerritsen M Hillan KJ, 2003-174141/17. A ME, CO. Botstein D, ij I A, GC. Eaton DL, Ferrara N, Filvaroff N, Godowski PJ, Grimaldi JC, Gu Napier MA, Roy MA, Tumas D, V Gurney AL; Wood WI;

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GENENTECH

N-PSDB;

New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.

Claim 12; Fig 32; 178pp; English.

The invention relates to an isolated PRO polypeptide (a secreted or CC transmembrane protein) comprising: (a) at least 80% sequence identity or CC positives when compared to any of 15 sequences, fully defined in the CC specification, lacking or with its associated signal peptide; or (b) at CC coding sequence of a DNA deposited in the American Type Culture CC coding sequence of a DNA deposited in the American Type Culture CC coding sequence of a DNA deposited in the American Type Culture CC coding sequence of a DNA deposited in the American Type Culture CC coding sequence or full-length coding sequence identity to a nucleotide sequence (C that encodes a PRO protein; (b) at least 80% sequence with any of 15 fully CC defined sequences of 957-3441 base pairs, given in the specification; or CC (c) at least 80% sequence identity to a full-length coding sequence of a CC DNA deposited under ATCC Accession No. 209526, 209527, 209528, CC 209530, 209523, 209422, 209532, 209531, 209529, 209570, 209518, CC 209530, 209523, 209422, 209532, 209531, 209529, 209570, 209518, CC 209530, 209531, 209523, 209531, 209527, 209540, a host CC cell comprising the vector comprising the nucleic acid; (3) a host CC comprising the vector which, when cultured under conditions suitable CC comprising the PRO polypeptide, produces the PRO protein; (4) a CC chimeric molecule comprising PRO fused to a heterologous amino acid compositions of cd disorders associated with the PRO polypeptide, such as AIDS (acmired CC disorders associated with the PRO polypeptide, such as AIDS (acmired disorders associated with the PRO polypeptide, such as AIDS (acquired immunodeficiency syndrome), cancer, atherosclerosis, inflammatory disease, diabetic complications, cardiac injury and organ failure. The

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17-CCT-1997;
05-NOV-1997;
12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
25-FEB-1998;
20-MAR-1998;
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biological assays.
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99WO-US030095.
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Ashkenazi i Ferrara N, Grimaldi J Roy MA, Zhang Z; Stewart TA, AJ, Baker KP, Botstein D, Desnoyers L, Eaton , Fong S, Gerber H, Gerritsen ME, Goddard A, JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Stewart TA, Tumas D, Watanabe CK, Williams PM, Godowski | Paoni NF; Wood WI; DL; PJ;

WPI; 2003-247083/24. N-PSDB; ABX80473.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer

Claim 12; Fig 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO CC polypeptides are useful in detecting PRO polypeptides in a sample, in CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and CC in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of meonatal heart and is thus CC useful for treating cardiac insufficiency disorders. PRO154 and PRO1186 CC stimulate advantal capillary endothelial growth, and PRO5136, CC PRO943, PRO828, PRO926, PRO1068 or PRO535, PRO826, PRO819, PRO8128, PRO826, PRO1068 or PRO535, PRO819, PRO81126, CC PRO943, PRO828, PRO926, PRO1068 or PRO535, PRO819, PRO81126, CC PRO943, PRO828, PRO926, PRO1068 or PRO535, PRO819, PRO81126, CC Useful for treating conditions or disorders where anglogenesis would be beneficial, e.g. wound healing and ancagonist of this polypeptide are CC useful for treating cancerous tumours. PRO812 inhibits vascular CC useful for treating cancerous tumours. PRO812 inhibits vascular CC cells and is thus useful for inhibiting endothelial cell growth in CC mammals which would be beneficial in inhibiting tumour growth. PRO826,

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RESULT 10
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                              Human; PRO; secreted protein; transmembrane protein; cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loretinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; here Crohn's disease; sports injury; arthritis
            Homo
                                                                                                                              Human
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                                    disease; nephropathy; dermatitis; herpetiformis;
injury; arthritis.
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99WO-US0211090
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2000WO-US00031665
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98US-0091528P.
98US-0091628P.
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98US-00916333.9P.
98US-0091633.9P.
98US-0091634.9P.

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RESULT 11
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13-NOV-1997
13-NOV-1997
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2000WO-US004414
2000WO-US004914
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98WO-US021141.
98WO-US025108.
99WO-US005028.
99WO-US012252.
99WO-US012252.
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang DL; Godowski l Paoni NF; Wood WI; P.

WPI; 2003-288106/28. N-PSDB; ABX90451.

New transmembrane polypeptides and nuo polypeptides, useful in gene therapy, chromosome markers, or in generating p nucleic acids encoding the py, in chromosome identification, probes

Claim 12; Fig 328; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polypureleotides are also useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for

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RESULT 12

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 16-JUN-1997;
17-OCT-1997;
05-NOV-1997;
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25-FEB-1998;
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Pred. No. 3.6e-173;
Mismatches 0;
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2000WO-US0021547
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2000WO-US0021547
2000WO-US0031565
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2000WO-US003157
2000WO-US003157
2000WO-US003131
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The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The PRO CC polypeptides are secreted and transmembrane proteins. The PRO CC polypeptides are useful for detecting other PRO polypeptides, for linking CC biological activities of cells expressing PRO polypeptides, and for for cc dentifying agonists or antagonists. The polynucleotide sequences cc encoding PRO polypeptides, and for for CC chromosome and gene mapping, in the generation probes, in CC chromosome and gene mapping, in the generation probes for mapping the green which encodes the PRO polypeptides, for generating transgenic animals of individuals with genetic disorders, in gene therapy, for chromosome cc identification, as chromosome markers, and for generating probes for PCR, CC Northern analysis, Southern analysis and Western analysis. ABU13860-CC ABU14006 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
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21-JUI-2000;
11-AUG-2000;
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24-AUG-2000;
08-NOV-2000;
01-DEC-2000;
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Grimaldi
Roy MA,
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Ferrara N,
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DB; ABX64297.
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                                                                                                                                                                                                                          MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ
                                                                                                               TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
                                                                                                                                                                                 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII
TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT
                              HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                                                 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                                                                                              TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
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2000WO-US023522

2000WO-US030352

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25-FEB-1998
16-SEP-1998
16-DEC-1998
16-DEC-1998
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28-JUL-2000; 2000WO-US020710.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
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Gerritsen M
Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New secreted and transmembrane polypeptides (e.g. PRO241, for use in pharmaceuticals, diagnostics or bioreactors, particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.
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N-PSDB; ABX89495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various industrial applications. Sequences ABU60230-ABU60245 represent human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a human secreted and transmembrane polypeptide (PRO) and the polymucleotide encoding it. The PRO polypeptide or polymucleotide is useful in pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating cancers, inflammatory diseases, atheroscierosis, cardiac injury,
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n ME, Goddard A,
J, Kljavin IJ, N
                                                                    EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
                                                                                                                              AVLTTTFQAPTDSKGSI
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                        DYLINGIYVDI
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, Godowski PJ, Grimaldi JC, Gurn
Napier MA, Roy MA, Tumas D, Woo
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Pred. No. 3.6e-173;
; Mismatches 0;
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RESULT 14

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97US-0062250P
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16-SEP-1998
17-SEP-1998
07-OCT 1998
07-OCT 1999
08-MAR 1999
08-MAR 1999
15-SEP-1999
11-SEP-1999
11-DEC-1999
11-DEC-1999
11-DEC-1999
11-DEC-1999
11-FEB-2000
11-FEB-2000
11-FEB-2000
12-FEB-2000
11-FEB-2000
11-FEB-2000
11-MAR-2000
The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
                                                                                                                                                                                                                                                                                         Ashkenazi
Ferrara N,
Grimaldi J
                                                                                                                                                                                                                                                                                                                                                                              29-JUN
09-JUL
28-AUG
                                                                                                                                                                                                                                                                 Roy M
Zhang
                                                                                                                              Claim
                                                                                                                                                                  New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kapos: parcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn
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)B; ACA64519.
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                                                                                                                             Fig
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99WO-US02831
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2000WO-US006319
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cancer, Kaposi's rosis or Crohn's

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2001US-00944944

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RESULT 15
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Matches 431
                                                                                                               Cornelia de L inflammatory infertility;
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                                                                                                    diabetic
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                                                                                                               PRO; secreted protein; transmembrane protein; ia de Lange syndrome; gene therapy; immune disorder; martory disease; organ failure; atherosclerosis; cardility; birth defect; premature aging; cardiac injury
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ilarity 100.0%;
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Pred. No. 3.6e-173;
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12-DEC-1997;
16-DEC-1997;
16-DEC-1997;
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2000WO-US003565.

2000WO-US005841.

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2000WO-US005849.

2000WO-US008439.

2000WO-US00871.

2000WO-US02071.

2000WO-US032678.

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2001US-00866028.
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98US-0074988P
98US-0075945P
98US-0075945P
98WO-US025108
98WS-0112850P
98US-0113256P
98US-0113258P
99WO-US012252
99US-0146222P
99WO-US028113
99WO-US028113
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(GETH) GENENTECH INC.

Baker KP, Botstein Gerritsen ME, Godda Hillan KJ, Kljavin Botstein D, Ea IJ, Eaton DL, Ferrara N, Filvaroff E; A, Godowski PJ, Grimaldi JC, Gurn Napier MA, Roy MA, Tumas D, Woo Gurney AL; Wood WI;

N-PSDB; 2003-311003/30. DB; ABX96832.

New transmembrane polypeptides and polynucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene or as molecular weight markers.

Claim 12; Fig 32; 172pp; English.

The invention relates to an isolated nucleic acid encoding a secreted/
CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and their encoding polynucleotides are disclosed. Also
CC included are a vector comprising the PRO nucleic acid, a host cell
CC comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an
CC isolated polypeptide having at least 80% amino acid sequence identity to
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptides, a chimaeric molecule sequence and an antibody which specifically binds
CC in chromosome and gene mapping, in generating sense and antisense RNA or
CC pNA, in generating transgenic or knock-out animals which can be used in
CC gene therapy. The polypeptides may be used as molecular weight markers
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
CC acids may also be used for chromosome identification, and tissue typing.
CC conditions are available to the proper consolidate gene for cornella de Lange
CC cornella de Lange syndrome. Other PRO proteins are variously implicated in immune disorders, inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, cardiac injury,

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                                                            EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
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Search completed: April 28, Job time: 63 secs 2004, 12:57:51

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Perfect score:
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-448-947-332

US-09-241-581B-6

PCT-US95-07721-6

US-08-700-651-12

US-08-928-361B-17

US-09-588-995A-17

US-09-588-995A-20

US-09-928-361B-20

US-09-145-473E-40

US-09-145-473E-40

US-09-216-393B-344

US-09-216-393B-344

US-08-471-970A-8

US-08-928-361B-5

US-08-928-361B-5

US-08-928-361B-5

US-09-588-995A-5

US-08-928-361B-6

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US-08-270-076A-1:
US-08-928-361B-1:
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Patent No.
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ALIGNMENTS

Application US/09866028

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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                       ; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-83
                                                                                                                                                                                                                                                                                                                     Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 120 SEQ ID NO 83
                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                           Matches
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Roy, Margaret
Tumas, Daniel
Wood, William
TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD
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Grimaldi, Christopher
Gurney, Austin
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Kljavin, Ivar
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Goddard, Audrey
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Filvaroff, Ellen
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Pred. No. 3.5e-202;
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GENERAL INFORMATION:
APPLICANT: ROSEN et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031p1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/094,657
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SOFTWARE: Patentin
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Query Match
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Patent No. 6476195
                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SITE
LOCATION: (97)
OTHER INFORMATION: )
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EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
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EARLIER FILING DATE: 1998-08-12
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 266
TYPE: PRT
ORGANISM: Homo sapiens
                                                         NAME/KEY: SITE
LOCATION: (206)
OTHER INFORMATION: Xaa
                                                                                                                    LOCATION: (199)
OTHER INFORMATION:
                                                                                                         FEATURE
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LOCATION: (199)
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LOCATION: (195)
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US-09-241-581B-6
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                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vere
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,581B
FILING DATE: 02-Feb-1999
CLASSIFICATION: <Unknown>
ATTORNEY/REENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                         FEATURE:
                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabet
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Massachusetts Institute of Technology TITLE OF INVENTION: Class BI and CI Scavenger Receptors NUMBER OF SEQUENCES: 8
                                                                                                                                                                         FEATURE
                                                                                                                                                                                                               HYPOTHETICAL: NO
                                                                                                                                                                                             FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 TQAVVDKTLLLVVLLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLINGMYAD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 LLPENVSALPATVAVASPHT-----TSATPKPATL-LPTNASV----TPS--GTSQPQLA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 TDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAH 217
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                                                                               NAME/KEY: misc. feature
LOCATION: 1.629
OTHER INFORMATION: /Function = "Amino acid sequence for the
Drosophila Melanogaster Scavenger Receptor
                                                                         Class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPPMX ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQA-PTDSKGSLETIPFTE 324
NAME/KEY: Modified LOCATION: 30..353 OTHER INFORMATION:
                                                                                                                                                                                                                                                                  TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EKWLLIGSLLEGVLELVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISHLTLHTGHVYNPTA---LSMSHVESSTMNKTASWEGREASPGSSSQGSVPENQYGLPF 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TALAQVPKSSALPRTATLATLATRA----OTVATTANTSSPMSTRPSPSKHMPSDTAASP
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                                                                                                                                                                                                                                                                                                                                                TELEFAX: (404)
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pabst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                             internal
                                   Modified-site
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 /note=
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 "Positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116;
 30-32,
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FEATURE:
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                                                                                                                                                                                                          NAME/KEY: Modified-site
LOCATION: 576..602
OTHER INFORMATION: /note= "Amino : 599-602 represent casein kinase II sites."
                                                                                                                590-592 represent protein kinase C
                                                                                                                                                                                                                                                                                                    represent a putative cytoplasmic domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement control protein domain number 1."
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Domain LOCATION: 565..629 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "Amin
represent a mucin-like potential
O-linked glycosylation region."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
LOCATION: 338.381
OTHER INFORMATION: /note= "Amino acids 338-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "The cysteines at positions 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216, 217, 254, 310, 339, 343, 361, 363, 367, 373, 374 and 381 represent potential disulfide linkages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 128..312
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site LOCATION: 75..127 OTHER INFORMATION: /note
                                                                                                                                               NAME/KEY: Modified-site LOCATION: 578..592
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                              VIDER INFORMATION: /note= "Amino acids represent a putative TM domain."
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Domain LOCATION: 544..564 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 22..381
OTHER INFORMATION:
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represent an MAM domain."
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129-131, 180-182, 253-255 and 351-353 represent potential N-glycosylation
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                                                                                                                                                                                                                                            /note= "Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acids 387-514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
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ol protein
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                                                                                                                                                                                                                                              576-579
                                                                                                                                                                                                                                                                                                                                                                                                                     544-565
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US-08-265-428-6
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                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MIT6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEPAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08265428
Patent No. 6429289
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: I
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,428
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Krieger, Monty
TITLE OF INVENTION: Class BI Scavenger Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                             NAME/KEY: Modified-site LOCATION: 30..353 OTHER INFORMATION: /note OTHER INFORMATION: 129-1
                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                    NAME/KEY: misc.
LOCATION: 1..62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 |
CITY: Atlanta
                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 QEIAHLLPENVSALPATVAVASPHT-----TSATPKPATLLPTNASVTPSGTSQ 261
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                                                                                                                                                                  feature
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22.9%; Pred. No. 5.7e-05;
ative 30; Mismatches 79
                                                                                                                                    /Function = "Amino
                                                 /note= "Positions 30-32, 90-92, 129-131, 180-182, 253-255 and 351-353
                               potential N-glycosylation sites
                                                                                                                                                                                                                                                                                                                                                                                                       31,284
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                                                                                                                                    acid
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                                                                                                                                    sequence
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NAME/KEY: Modified-site
LOCATION: 596..599
OTHER INFORMATION: /note= "Amino acids 596-599
OTHER INFORMATION: represent a CAMP protein kinase site.
US-08-265-428-6
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Domain
LOCATION: 565.629
OTHER INFORMATION: repressible for the control of the control
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OTHER INFORMATION: A putat:
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..74
OTHER INFORMATION: compleme
FEATURE:
NAME/KEY: Modified-site
LOCATION: 75..127
OTHER INFORMATION: compleme
FEATURE:
NAME/KEY: Modified-site
LOCATION: 75..127
OTHER INFORMATION: 2."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 128..312
OTHER INFORMATION: represe:
FEATURE:
NAME/KEY: Modified-bond
LOCATION: 2..381
OTHER INFORMATION: 22.45,
OTHER INFORMATION: 22.45,
OTHER INFORMATION: 22.45,
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LOCATION: 578..592
OTHER INFORMATION: /note
OTHER INFORMATION: 590-5
    262
                                                                                 383
                                                                                                                                                                  213
PQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIP 321
                                                                            KELLTTTEDDISSLPPTVTSTSTSTTRKSTTTTTSTTTTSTTTTKRPTTTTTKATTT
                                                                                                                                                             QEIAHLLPENVSALPATVAVASPHT-----TSATPKPATLLPTNASVTPSGTSQ 261
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                      6.6%; Score 145.5; DB 4; 22.9%; Pred. No. 5.7e-05; tive 30; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "
599-602
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represent a mucin-like potential O-linked
glycosylation region."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "The cysteines at positions 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 217, 254, 310, 339, 343, 361, 363, 367, 373, represent potential disulfide linkages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Amino acids 578-580 and 590-592 represent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Amino acids 128-312 represent an MAM domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Amino acids 21-74 protein complement control protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Amino acids 544-565 represent a putative TM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Amino acids 1-20 re
a putative signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acids 565-629
represent a putative cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino represent a so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Amino acids 576-579 and represent casein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nino acids 75-127 complement control protein domain number
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somatomedin B domain."
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	Db	496TIMIPTSSTEKTIGIITTMKTRKRITWNVDPQDIEGHMDTSGSTPNPALV- 54
	γQ	375 NQYGLPFEKWLLIGSLLFGVLFLVIGLVLL 404
	Db	547VLYLLLGIVLV 557
	RESUL	RESULT 5
	PCT-U	Sequence 6, Application PC/TUS9507721
	, .	INFORMATION: ANT: Massachus
		CI Sc
		PONDENČE ADDRESS
		2800 One Atlantic Ce
		STREET: 1201 West Peachtree Street CITY: Atlanta
		STATE: Georgia
	٠. ٠	ZIP: 30309-3450
		ER READABI
·	٠	BM PC compatible
	·· ··	SOFTWARE: Patentin Release #1.0, Version #1.25
	•••	APPLICATION NUMBER: PCT/US95/07721
		CLASSIFICATION:
		ATTORNEY/AGENT INFORMATION: NAME: Pabst, Patrea L.
	. •.	REGISTRATION NUMBER: 31,284
	•••	ż
		TELEPHONE: (404) 873-8794 TELEFAX: (404) 873-8795
	, in	N FOR SEQ
		LENGTH: 629 amino acids
		TYPE: amino acid TOPOLOGY: linear
		MOLECULE TYPE: protein
		FRAGMENT TYPE: internal
	•• ••	EY:
	. ~.	INFORMATION: /Finction = "Amino acid
	** *	a Melanogaster Scavenger Rec
	~. ~.	INFORMATION: Class CI."
	·• •• ·	
	•. •	DRMATION: /note= "Positions 30-3
	· ••• •	INFORMATION: 129-131, 180-182, 25
	·· ··	INFORMATION: represent sites."
		FEATURE: NAME/KEY: Modified-site
		ION: 120
	·	OTHER INFORMATION: /NOTHER INFORMATION: a putative signal sequence."
		Modified-site
		LOCATION: 2174 OTHER INFORMATION: /note= "Amino acids 21-74 represent

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                                                                                                                                Query Match
Best Local Similarity
Matches 48; Conserv
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OTHER INFORMATION: 1/
FEATURE:
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NAME/KEY:
LOCATION:
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OTHER INFORMATION: /notesOTHER INFORMATION: represOTHER INFORMATION: O-link
                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
LOCATION: 578..592
OTHER INFORMATION: /note=
OTHER INFORMATION: 590.59
OTHER INFORMATION: sites.
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site LOCATION: 576..602 OTHER INFORMATION: /note=OTHER INFORMATION: 59-60 OTHER INFORMATION: sites.
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LOCATION: 565.629
OTHER INFORMATION: /
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OTHER INFORMATION: /
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LOCATION: 22..381
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 596..599
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LOCATION:
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 443
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                                                                                                  213 QEIAHLLPENVSALPATVAVASPHT-----TSATPKPATLLPTNASVTPSGTSQ 261
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                              PQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIP 321
KRTTTTKKPTTTSTTPKPTTTTSTTPKSTTSTTSTTPTTTTTTINVFTTKK-----
                                                                KELLITTEDDISSLPPIVISTSTSTRKSTTTTTSTTTTSTTTTKAPTTTTTTKATTT
                                                                                                                                   Conservative
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                                                                                                                                                  6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Amino acids 387-514
represent a mucin-like poter
O-linked glycosylation region
                                                                                                                                                                                                                                                                                                       /note= "Amino acids 578-580 and
590-592 represent protein kinase C
sites."
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Amino acids 576-579 and
599-602 represent casein kinase
sites."
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                                                                                                                                                                                                                    /note= "Amino acids 596-599 represent a cAMP protein ki
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domain num
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number 1."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Amino acids 565-629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Amino acids 544-565
represent a putative TM domain."
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                                                                                                                              30; Mismatches
                                                                                                                                  Score 145.5; DB 5;
Pred. No. 5.7e-05;
0; Mismatches 79;
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                                                                                                                                                                                                                       kinase site."
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APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSEPOTIGHEM PARVUM
TITLE OF INVENTION INFECTIONS
TITLE OF INVENTION UMMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-08-14
SACID NO 12
SEQ ID NO 12
LENGTH: 175
TYPE: PRT
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-928-361B-17
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Best Local Similarity
Matches 35; Conserve
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US-08-700-651-12
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                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Petersen, (
TITLE OF INVENTION: PI
TITLE OF INVENTION: FI
TITLE OF INVENTION: SI
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APPLICANT: PETERSEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08700651B Patent No. 6015882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Cryptosporidium parvum FEATURE:
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY,
                                                                          CITY:
STATE:
                                                                                                                 STREET:
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                                                                                           Palo Alto
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                                                                                                           385 Sherman Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                     , Carolyn
PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
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27.3%;
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Pred. No. 0.00027;
5; Mismatches 74
                                                                                                                 JONES & BIKSA
e, Suite 6
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TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-5
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/28,361
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR PILING DATE: 1995-04-03
NUMBER: 07 SEQ ID NOS: 115
; TYPE: PRT ; ORGANISM: Cryptosporidium parvum US-09-588-995A-17
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US-09-588-995A-17
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; MOLECULE TYPE:
US-08-928-361B-17
                                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6514697
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
                                                          LENGIH: 175
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 12-SEF CLASSIFICATION:
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35; Conserv
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NELSON, RICHARD C.
GUT, JIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09588995A
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12-SEP-1997
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Pred. No. 0.00027
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; Sequence 20, Application US/08928361B
; Patent NO. 6071518
; GENERAL IMPORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYP;
TITLE OF INVENTION: THEIR FUNCTIONA;
TITLE OF INVENTION: FOR TREATMENT AFTITLE OF INVENTION: SPECIES INFECTION;
TITLE OF INVENTION: SPECIES INFECTION;
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APPLICANT: ESTERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: MILSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND I
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIGHUM PARVUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1995-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
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SEQ ID NO 15
LENGTH: 249
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Best Local Similarity 27.3%;
Matches 35; Conservative 1
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    NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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o. 6015882
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, Carolyn
PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
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Pred. No. 0.00027;
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RESULT 11
US-09-588-995A-20
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                                                     APPLICANT: GUT, JIRI

APPLICANT: GUT, JIRI

TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

FILE REFERENCE: 480.19-5

CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT FILING DATE: 2000-06-06

PRIOR APPLICATION NUMBER: 08/827,171

PRIOR FILING DATE: 1997-03-27

PRIOR FILING DATE: 1997-03-27
                                  PRIOR
PRIOR
                                                                                                                                                                                                       APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
7/0 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES &
STREET: 385 Sherman Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 1
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REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
FILING DATE: 1996-08-14
                 APPLICATION NUMBER: 08/700,651
                                  APPLICATION NUMBER: 08/928,361 FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                             INFORMATION:
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13-SEP-1996
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26.0%;
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Pred. No. 0.00059;
5; Mismatches 82
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US-09-345-473E-40
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SEQ ID NO 40
LENGTH: 1601
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Patent No. 6558903
GENERAL INFORMATION:
APPLICANT: Hodge, Martin
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 249
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Matches 83; Conserv
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CURRENT FILING DATE: 1999-06-30
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ORGANISM: Cryptosporidium parvum
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                                 ---LTTTFQAPTDSKGSLETIPFTEISNLTLNT-GNVYNPT-ALSMSNVESSTM-----
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                                                                                                                                                                                                                                                                                                                          KGL-MSYRIITDFPS--LTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISW 168
APFKTEDIQTPTLAQNTVPRTISTDASGLVINTPASIASPSPAPSATDVASTTAPVTPAP
                                                                     NIPAMSPTSAQPQPVLSPTSAAVPVPTTMIH-VPKPSEIPVQNVÄTTAAPVAANNVPPSP
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Pred. No. 0.00059;
                                                                                                       --PTTLISTVFTRAAATLQAMATTAV------
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US-09-216-393B-344
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US-09-216-393B-341
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APPLICANT: Milhausen, Michael James
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES,
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 344
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SEQ ID NO 341
LENGTH: 288
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Best Local Similarity
                                                                                                  Query Match
Best Local Similarity
                                                                                 Matches 44;
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEF
FILE REFERENCE: TX-1-C2
                                                                                                                                                                               TYPE: PRT
ORGANISM: Toxoplasma
                                                                                                                                                                                                                        LENGTH: 288
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                                       178 SSDHLEKLFKMDEAS-------AQLLAYKEKGHSQSSQFSSDQEIAHLLPE 221
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  STDAIDRVSQFDLVSLLDVIREAAQAKFDLLGRLITDIASGIGEGAMALMGEEAAFIRPR 138
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                                                                                 Conservative
                                                                                                                                                                                                                                                                  version 3.1
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                                                                                               5.7%; Score 127; DB 4;
21.2%; Pred. No. 0.00093;
                                                                             33; Mismatches 109;
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/078,683 FILING DATE: 17-JUN-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Saunde
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
TOPOLOGY: line
WOLECUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Kato, Masato
TITLE OF INVENTION: Construction and USe of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                            y Match 5.7%; Score 127; DB 1; Length 357;
Local Similarity 26.3%; Pred. No. 0.0013;
hes 67; Conservative 25; Mismatches 109; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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                                                          250 ----TNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLT- 304
                                                                                                                                           219 LPENVSALPATVAV------
                                                                                                                                                                                                                        159 DYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHL
                                                                                                    87
                                                                                                                                                                                   41 NYERPVDLE------GSGD--DDPFGDDELDD---AYSGSGSGYFEQESGLETAVSL
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                      TTASTTASDSPSTTS--TTTTTAATTTTTTTTTTSTTVATSKPTTTQRFLPPFVTKAATTR 204
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Search c Job time	ъ	8	Db	φ
Search completed: April 28, 2004, 13:00:26 Job time : 25 secs	262 PTTLPPTEAPQVEPG 276	364 PGSSSQGSVPENQYG 378	205 ATTLETPTTSIPETSVLTEVTTSRLVPSSTAKPRSLPKPST-SRTAEPTEKSTALPSS 261	305 -TTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREAS 363

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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2211
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Copyright (c) 1993 - 2004 Compugen Ltd
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/cgn2_6/ptodata/1/pubpaa/US099_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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23	Sequence 515, App		Sequence 83, Appl	Sequence 515, App	Sequence 515, App		Sequence 83, Appl	Sequence 515, App	Sequence 83, Appl	Sequence 515, App	•		۲.	Sequence 83, Appl	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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51	51	51	51	Sequence 515, App	51	e 51	515	515	83,	515	515	83,	515	515,	515,	83,	83,		515,	83,	83,	515,	83,	æ	83,	515	Sequence 515, App	Sequence 83, Appl	Sequence 83, Appl

ALIGNMENTS

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 83
SEQ ID NO 83
TYPE: PRT
ORGANISM: Homo Sapien
US-09-866-028-83
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US-09-866-028-83
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Patent No. US20020058399A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
Query Match 100.0%; Score 2211; DB 9; Length 431; Best Local Similarity 100.0%; Pred. No. 1.3e-179; Matches 431; Conservative 0; Mismatches 0; Indels 0
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APPLICANT:
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                                                                                                                                                                                                                                                                                                         Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul
Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                  Kljavin, Ivar
                                                                                                                                                                                                                                                                                                                                                                                                      Hillan, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen, Mary
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Bemoyers, Luc
APPLICANT: Bemoyers, Luc
APPLICANT: Ferrara, Rapoleone
APPLICANT: Ferrara, Rapoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Germaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Mapier, Mary A.
APPLICANT: Rodowski, Paul J.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Daniel
APPLICANT: Wood, William I.
APPLICANT: W
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Patent No
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OR APPLICATION NUMBER: 60/078910
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RESULT 3
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; Sequence 515, Application US/09989723
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Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Apvid
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspett
APPLICANT: Goddwski, Pauli
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OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
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OR FILING DATE: 1998-07-07
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Eaton, Dan L.

Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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OR FILING DATE: 1997-06-16
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OR FILING DATE: 1997-11-12
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OR PELLING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/065311
OR PELLING DATE: 1997-11-24
OR PELLING DATE: 1997-11-24
OR PELLING DATE: 1998-02-25
OR FILING DATE: 1998-03-20
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OR PELLING DATE: 1998-03-20
OR PELLING DATE: 1998-03-20
OR PELLING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/08322
OR FILING DATE: 1998-05-28
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OR APPLICATION NUMBER: 60/08706
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Pan, James
Paoni, Nicholas F.
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art, Timothy A.
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947 : 1998-06-18 NUMBER: 60/ 1998-06-19 1998-06-17 1998-06-19 1998-06-17 1998-06-17 1998-06-17 1998-06-17 1998-06-17 60/089948 60/089907 60/089801 60/089653 60/089600 60/089599 60/089598 60/089538 60/089532 60/089952

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OR APPLICATION NUMBER: 60/091633
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                                                               AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR
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APPLICANT: Williams, P. Mickey
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APPLICANT: Education Milliams I.
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APPLICATION INTEREST: US/9989,279
CURRENT APPLICATION NUMBER: US/9489,279
CURRENT FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06220
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/075945
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Gerber, Hanspeter
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Kljavin, Ivar J.
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Eaton, Dan L.
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Botstein, David
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                                                                    FILE REFERENCE: P2730P1C65

CURRENT APPLICATION NUMBER: US/09/989,727

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR PLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/06511

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/066770

PRIOR PILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1998-02-25

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PRIOR APPLICATION NUMBER: 60/078910

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
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5. US20020072497A1
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Gerritsen, Mary E
Goddard, Audrey
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Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood, William I.
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                             : 1998-03-20
NUMBER: 60/083322
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OR APPLICATION NUMBER: 60/088810
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OR FILING DATE: 1998-06-10
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OR APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088029
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APPLICANT: Bater, Kevin
APPLICANT: Bater, Kevin
APPLICANT: Botstein, David
APPLICANT: Betrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,449
CURRENT ELING DATE: 2001-05-26
PRIOR FILLNG DATE: 2001-05-26
PRIOR APPLICATION NUMBER: 60/067,411
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OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-09
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Pred. No. 1.3e-179;
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ICR APPLICATION NUMBER: 60/069,702
ICR FILING DATE: December 16, 1997
ICR APPLICATION NUMBER: 60/069,870
ICR APPLICATION NUMBER: 60/069,870
ICR APPLICATION NUMBER: 60/069,870
ICR FILING DATE: December 17, 1997
ICR APPLICATION NUMBER: 60/068,017
ICR FILING DATE: December 18, 1997
ICR FILING DATE: December 18, 1997
ICR FILING DATE: January 5, 1998
ICR APPLICATION NUMBER: 60/074,098
ICR APPLICATION NUMBER: 60/074,098
ICR APPLICATION NUMBER: 60/074,098
ICR APPLICATION NUMBER: 60/075,945
ICR FILING DATE: February 9, 1998
ICR APPLICATION NUMBER: 60/112,850
ICR APPLICATION NUMBER: 60/112,850
ICR APPLICATION NUMBER: 60/113,296
ICR APPLICATION NUM
                                                                                                                                                                                                                                                                                                          OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: No. US20020102647ALember 30
OR APPLICATION NUMBER: PCT/US99/2813
OR APPLICATION NUMBER: PCT/US99/2813
OR FILING DATE: No. US20020102647ALember 30
OR APPLICATION NUMBER: PCT/US99/28301
OR FILING DATE: December1, 199
OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: December 16, 199
OR APPLICATION NUMBER: PCT/US00/0365
OR APPLICATION NUMBER: PCT/US00/04414
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R FILING DATE: December 11, 1997
DR APPLICATION NUMBER: 60/069,425
PR FILING DATE: December 12, 1997
DR APPLICATION NUMBER: 60/069,696
DR FILING DATE: December 16, 1997
DR APPLICATION NUMBER: 60/069,694
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
FILING DATE: September 15, 1999
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FILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
                                                       FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
                                                                                                                                                                   FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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US-09-944-449-83
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Patent No. US:20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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                                 Stewart, Timo
Tumas, Daniel
                                                Roy, Margaret Ann
Stewart, Timothy A.
                                                                           Pan, James
Paoni, Nicholas F.
                                                                                                   Napier, Mary A.
                                                                                                                Gurney, Austin L. Kljavin, Ivar J.
                                                                                                                                         Godowski, Paul J.
Grimaldi, J. Christopher
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Goddard, Audrey
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Gerber, Hanspeter
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Pred. No. 1.3e-179;
'; Mismatches 0;
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Watanabe, Coli Williams, P. M Wood, William

Colin K. P. Mickey

OR APPLICATION NO OR FILING DATE: 1 OR APPLICATION NO OR FILING DATE: 1 OR APPLICATION NO OR APPLICATI	 PRIOR APPLICATION NUMBER: 60/08861 PRIOR APPLICATION NUMBER: 60/088876 PRIOR APPLICATION NUMBER: 60/088876 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/089105 PRIOR FILING DATE: 1998-06-16 PRIOR PPLICATION NUMBER: 60/089512 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089514 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089539 PRIOR APPLICATION NUMBER: 60/089539 PRIOR APPLICATION NUMBER: 60/089599 PRIOR APPLICATION NUMBER: 60/089599 PRIOR APPLICATION NUMBER: 60/089599 PRIOR APPLICATION NUMBER: 60/089599 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089600 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089600 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089907 PRIOR APPLICATION NUMBER: 60/089907 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089907 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089908

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US-09-44-457-83
US-09-944-457-83
; Sequence 83, Application U
; Patent No. US20020110859A1
; GENERAL INFORMATION:
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Matches 431;
APPLICANT: Baker, Kevin APPLICANT: Botstein, David APPLICANT: Eaton, Dan
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OR APPLICATION NUMBER: 60/090695
OR FILING DATE: 1998-06-25
OR PILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090862
OR FILING DATE: 1998-06-26
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-07-06
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091544
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/092182
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Pred. No. 1.3e-179;
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APPLICANT: FETTERS, Mapoleone
APPLICANT: Gedraftsen, Mary
APPLICANT: Goddowski, Paul
APPLICANT: Mans Daniai
APPLICANT: Numes Daniai
APPLICANT: Nood, Milliam
APPLICANT:
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; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo S
US-09-944-457-83
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US-09-944-862-83
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Sequence 83, Application US/09944862
Patent No. US20020115145A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
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OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/20710
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US00/32678
OR FILING DATE: December 1, 2000
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OR APPLICATION NUMBER: PCT/US99/28301
OR FILING DATE: December1, 1999
OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: December 16, 1999
OR APPLICATION NUMBER: PCT/US00/03565
OR FILING DATE: February 11, 2000
OR FILING DATE: February 11, 2000
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FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
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NUMBER: PCT/US99/28301
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Pred. No. 1.3e-179;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: 09/666,028
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR APPLICATION NUMBER: 60/111,285
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR APPLICATION NUMBER: 60/113,296
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PRIOR APPLICATION NUMBER: 60/113,296
PRIOR APPLICATION NUMBER: 60/113,2
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APPLICANT:
APPLICANT:
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R APPLICATION NUMBER: 1
R FILING DATE: June 22
R APPLICATION NUMBER: 1
RAPPLICATION NUMBER: PCT/US99/21090
FILING DATE: No. US2002011514 APPLICATION NUMBER: PCT/US99/28409
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Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
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Filvaroff, Ellen
Gerritsen, Mary
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E: December 16, 1998
N NUMBER: 09/218,517
E: December 22, 1998
N NUMBER: 09/254,311
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WMBER: PCT/US99/21090
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RESULT 10
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PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR PILING DATE: December 1, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PEDTUARY 11, 2000
PRIOR PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PELICATION NUMBER: PCT/US00/05841
PRIOR PILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR PILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
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GENERAL INFORWATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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LENGTH: 431
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ORGANISM: Homo Sapien
-09-944-862-83
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Eaton, Dan L.
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OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090678
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OR APPLICATION NUMBER: 60/090694
OR FILING DATE: 1998-06-25
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090695
OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/091360
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091514
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
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OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090445
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090472
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090535
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
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Pred. No. 1.3e-179;
; Mismatches 0;
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DR FILING DATE: 1998-06-05
RAPPLICATION NUMBER: 60/08212
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DR PILING DATE: 1998-06-05
DR APPLICATION NUMBER: 60/08855
DR FILING DATE: 1998-06-10
RAPPLICATION NUMBER: 60/088734
DR FILING DATE: 1998-06-10
PR APPLICATION NUMBER: 60/088736
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088742
DR FILING DATE: 1998-06-10
RAPPLICATION NUMBER: 60/088810
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088826
DR FILING DATE: 1998-06-11
FILING DATE: 1998-06-11
PR APPLICATION NUMBER: 60/088856
DR FILING DATE: 1998-06-11
DR APPLICATION NUMBER: 60/08961
DR APPLICATION NUMBER: 60/08961
DR APPLICATION NUMBER: 60/08951
DR APPLICATION NUMBER: 60/08953
DR FILING DATE: 1998-06-15
DR APPLICATION NUMBER: 60/08953
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DR APPLICATION NUMBER: 60/09955
DR FILING DATE: 1998-06-22
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DR FILING DATE: 1998-06-23
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EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD Gaps 240 180 120 120 60 300 300 240 180 0

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FILE REFERENCE: P273 DPLC15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR APPLICATION NUMBER: 60/087607
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C15
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Gerritsen, Mary E
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Godowski, Paul
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  : 1998-06-02
NUMBER: 60/
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R FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/0
OR FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-10
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OR REPLICATION NUMBER: 60/08
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/08
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/08
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/08
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/08
OR FILING DATE: 1998-06-18
OR FILING DATE: 1998-06-18
OR FILING DATE: 1998-06-18 DR APPLICATION NUMBER: 60/088810
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088824
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088826
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088858
DR APPLICATION NUMBER: 60/088858 DR FILING DATE: 1998-06-05

DR APPLICATION NUMBER: 60/088212

DR AFPLICATION NUMBER: 60/088217

DR APPLICATION NUMBER: 60/088217

DR FILING DATE: 1998-06-05

DR APPLICATION NUMBER: 60/088655 DR FILING DATE: 1998-06-04

RAPPLICATION NUMBER: 60/088326

DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088167

DR FILING DATE: 1998-06-05

DR APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738 APPLICATION NUMBER: 60/088030 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04 60/089908 60/089801 60/089600 60/089598 60/089538 60/089514 60/089512 60/088876 60/088861 60/088742 60/088025 60/089947 60/089907 60/089653 60/089599 60/089532 60/089440 60/089105 60/088029 60/088028 60/088021

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 431; Conservative 0
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OR APPLICATION NUMBER: 60/09044
OR APPLICATION NUMBER: 60/09044
OR APPLICATION NUMBER: 60/09047
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OR APPLICATION NUMBER: 60/09053
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/09054
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OR APPLICATION NUMBER: 60/09057
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/09067
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OR APPLICATION NUMBER: 60/09067
OR APPLICATION NUMBER: 60/09069
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/09069
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/09069
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/091863
OR APPLICATION NUMBER: 60/091863
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/09163
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DR APPLICATION NUMBER: 60/090429

RFILING DATE: 1998-06-24

DR PELICATION NUMBER: 60/090431

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090435
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R APPLICATION NUMBER: 60/08
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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              0
           Score 2211; DB 9;
Pred. No. 1.3e-179;
; Mismatches 0;
                                                                Length
           Indels
                                                                431;
           0
           Gaps
           0
APPLICANT: Bater; Kevin
APPLICANT: Bater; Kevin
APPLICANT: Bater; Kevin
APPLICANT: Bater, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Hillan, Kenneth
APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Nood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT APPLICATION NUMBER: 09/86,028
PRIOR APPLICATION NUMBER: 09/86,028
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/063,334
PRIOR APPLICATION NUMBER: 60/063,334
PRIOR APPLICATION NUMBER: 60/063,334
PRIOR APPLICATION NUMBER: 60/063,278
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PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/063,278
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PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/063,696
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US-09-945-587-83
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No. US2002017
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LENGTH: 431
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IOR FILING DATE: February 22, 2000
IOR APPLICATION NUMBER: PCT/US00/05841
IOR FILING DATE: March 2, 2000
IOR APPLICATION NUMBER: PCT/US00/08439
IOR FILING DATE: March 30, 2000
IOR APPLICATION NUMBER: PCT/US00/10442
IOR FILING DATE: May 22, 2000
IOR APPLICATION NUMBER: PCT/US00/20710
IOR APPLICATION NUMBER: PCT/US00/20710
IOR APPLICATION NUMBER: PCT/US00/32678
IOR APPLICATION NUMBER: PCT/US01/06520
IOR FILING DATE: JULY 28, 2000
IOR APPLICATION NUMBER: PCT/US01/06520
IOR FILING DATE: February 28, 2001
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
APPLICATION NUMBER: 09/218,517
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
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APPLICATION NUMBER: PCT/US99/12252
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APPLICATION NUMBER: 09/254,311
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APPLICATION NUMBER: 60/074,092
APPLICATION NUMBER: 9, 1998
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FILING DATE: January 5, 1998
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APPLICATION NUMBER: 60/069,870
FILING DATE: December 17, 1997
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APPLICANT: Wattanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/062186
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Baker, Kevin P.
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Tumas, D
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Gerritsen, Mary E.
Goddard, Audrey
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Stewart, Timothy A.
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Ferrara, Napoleone
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PRIOR

DR APPLICATION NUMBER: 60/08511
DR APPLICATION NUMBER: 60/06770
DR FILING DATE: 1997-11-34
DR APPLICATION NUMBER: 60/06770
DR FILING DATE: 1998-02-25
DR APPLICATION NUMBER: 60/075945
DR FILING DATE: 1998-02-25
DR APPLICATION NUMBER: 60/08332
DR APPLICATION NUMBER: 60/084600
DR FILING DATE: 1998-05-07
PRILING DATE: 1998-05-07
PRILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/087609
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/087609
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/087609
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/080759
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/08025
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/08026
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/08026
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/08021
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RESULT 14
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OR APPLICATION NUMBER: 60/091478
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091544
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/092182
OR APPLICATION NUMBER: 60/092182
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-09
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                                                                                                                                 : Ashkenazi, Avi J.
: Baker, Kevin P.
: Botstein, David
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Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                        AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR
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                                                                                                         Desnoyers, Luc
Eaton, Dan L.
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Pred. No. 1.3e-179;
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APPLICANT: Zhang, Zemin Title OF INVENTION: Secreted and Transmet Title OF INVENTION: Acids Encoding the FILE REFERENCE: P2730P1C17

FILE REFERENCE: P2730P1C17

CURRENT APPLICATION NUMBER: 00/049787

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/06250

PRIOR PILING DATE: 1997-11-12

PRIOR PPLICATION NUMBER: 60/065311

PRIOR PPLICATION NUMBER: 60/065311

PRIOR PPLICATION NUMBER: 60/065311

PRIOR PPLICATION NUMBER: 60/065311

PRIOR PILING DATE: 1997-11-12

PRIOR PPLICATION NUMBER: 60/065311

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/075945

PRIOR PILING DATE: 1998-03-20

PRIOR PPLICATION NUMBER: 60/083322

PRIOR APPLICATION NUMBER: 60/087106

PRIOR PILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087106

PRIOR PILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: 60/087609

PRIOR PILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: 60/087609

PRIOR PILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR APPLICATION NUMBER: 60/087759

PRIOR APPLICATION NUMBER: 60/087609

PRIOR APPLICATION NUMBER: 60/087609

PRIOR APPLICATION NUMBER: 60/087609

PRIOR APPLICATION NUMBER: 60/087609

PRIOR APPLICATION NUMBER: 60/088021

PRIOR APPLICATION NUMBER: 60/088021

PRIOR APPLICATION NUMBER: 60/088025

PRIOR APPLICATION NUMBER: 60/088026

PRIOR PRILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR APPLICATION NUMBER: 60/088026

PRIOR APPLICATION NUMBER: 60/088026

PRIOR PRILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

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Pan, James
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art, Timothy A.
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/0

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OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/09057
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090678
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090690
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OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-25
OR FILING DATE: 1998-06-25
OR FILING DATE: 1998-06-26
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/090862
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091544
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/09163
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                                                                EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
                                                                                          EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
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Pred. No. 1.3e-179;
Mismatches 0;
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DR FILING DATE: 1998-06-10
PAPPLICATION NUMBER: 60/088824
PRILING DATE: 1998-06-10
PR APPLICATION NUMBER: 60/088826
PRILING DATE: 1998-06-11
PR APPLICATION NUMBER: 60/088861
PR FILING DATE: 1998-06-11
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PR FILING DATE: 1998-06-12
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PR APPLICATION NUMBER: 60/08951
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PR APPLICATION NUMBER: 60/09045
PR APPLICATION NUMBER: 60/09055
PR APPLICATION NUMBER: 60/09045
PR APPLICATION NUMBER: 60/09055
PR APPLICATION NUMBER: 60/090

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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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                                                                                                                                              DR FILING DATE: December 18, 1997
DR APPLICATION NUMBER: 60/070,440
DR FILING DATE: January 5, 1998
DR APPLICATION NUMBER: 60/074,086
DR FILING DATE: February 9, 1998
DR APPLICATION NUMBER: 60/074,092
DR FILING DATE: February 9, 1998
DR APPLICATION NUMBER: 60/075,945
DR FILING DATE: February 25, 1998
DR APPLICATION NUMBER: 60/112,850
DR FILING DATE: December 16, 1998
DR APPLICATION NUMBER: 60/112,850
DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 60/113,980
DR APPLICATION NUMBER: 60/113,980
DR APPLICATION NUMBER: 60/113,280
DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 60/13,296
DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 60/146,222
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FILING DATE: December 16
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FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069, FILING DATE: December 17, 1
                                                                                                            FILING DATE: July 28, APPLICATION NUMBER: P
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Grimaldi,Christopher
Gurney,Austin
Hillan,Kenneth
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Tumas, Daniel
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                                                                 : September 16, 1998
NUMBER: PCT/US98/25108
                      NUMBER: 09/216,
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PRIOR APPLICATION NUMBER: 09/218,517
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: March 3, 1999
PRIOR PILING DATE: March 3, 1999
PRIOR PILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/2409
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: No. US20020132766Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: No. US20020132766Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: No. US20020132766Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: December1, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: DECEMBER: PCT/US99/30095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Homo Sapien US-09-945-015-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID SEQ ID NO 83
LENGTH: 431
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OR FILING DATE: MARCH 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: MAY 22, 2000
OR APPLICATION NUMBER: PCT/US00/20710
OR FILING DATE: July 28, 2000
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US00/32678
OR FILING DATE: December 1, 2000
OR FILING DATE: December 1, 2000
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Local Similarity 100.0%;
nes 431; Conservative (
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APPLICATION NUMBER: PCT/US00/04414
FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/06520 FILING DATE: February 28, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDCINSCCSTKNISGDKACNLMIFDTRKTAROPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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                                   EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
                                                                                                                                                                       AVLTTTFQAPTDSKGSLETI PFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR
                                                                                                                                                                                                                                                                    TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT
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EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
                                                                                                                                   AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR
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Pred. No. 1.3e-179;
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360 360 300 300

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Db 421 DYLINGIYVDI 431

Search completed: April 28, 2004, 13:01:26
Job time : 50 secs

OM protein - protein search, using sw model

April 28, 2004, 12:55:48; Search time 21 Seconds (without alignments) 1974.217 Million cell updates/sec

Run on:

Title: Perfect score: Sequence:

Scoring table: US-10-677-471-83 2211 1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

_	hypothetical prote	T25697	9 2	122	6.2	136.5	29
Ş	gastric mucin (clo	I47141	8 2	528	6.2	137	28
	ascites sialoglyco	A53577	0	163	6.2	137.5	27
무	LDL receptor 2 pre	QRXLL2		90	6.2	138	26
	hypothetical prote	T33369	5 2	1275	6.3	140	25
Ş	mucin - rat	S24169		29	6.3	140	24
	hypothetical prote	T34369	7 2	1777	6.4	141	23
뫄	probable membrane	S57180	2	116	6.4	141.5	22
	membrane glycoprot	T45463		867	6.4	142.5	21
8	membrane glycoprot	T45462		98	6.4	142.5	20
	melanoma antigen h	A49179	1 2	491	6.4	142.5	19
da da	mucin 7 precursor,	A48018		377	6.4	142.5	18
	Pmel 17 protein -	S53871	6 2	626	6.5	143	17
5	probable membrane	S59310	4 2	1104	6.5	144.5	16
	mucin 6, gastric (B46629	5 2	50	6.5	144.5	15
뮹	serine proteinease	A47547	6 1	786	6.6	146	14
	mucin FIM-C.1 - Af	A45155	2	662	6.6	147	13
5	probable membrane	S25345 '	9	1609	6.7	147.5	12
	hypothetical prote	T34293		790	6.7	147.5	11
8	mucin MUC5B, trach	T45025	0 2	3570	6.8	149.5	10
	mucin 2 precursor,	A43932	0	3020	6.8	149.5	9
Ş	chitinase (EC 3.2.	JC4566	0 2	860	6.8	150.5	8
	glycoprotein X pre	VGBEX1		79	6.8	150.5	7
뭥	hypothetical prote	T21389	1 2	1251	6.9	151.5	6
	serine-rich protei	T39903	2	53	7.0	154	5
Ş	hypothetical prote	T22696		85	7.0	154.5	4.
	hypothetical prote	T22808		770	7.0	155.5	ω
3	mucin 5AC (clone J	S53362	7 2	47	7.3	160.5	2
В.	hypothetical prote	T29634	5 2	825	7.9	174.5	ם
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324 EISNLTLNTGNVYNPTALSMSNVESSTMNKTA 355

131	132	133	133	133	133	133	133.5	133.5	134	135.5	135.5	135.5	135.5	136	136
5.9	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.1	6.2	6.2
725	1162	1367	1075	636	610	556	3507	708	164	2271	1299	543	322	796	503
N	N I	N	N	Ņ	N	N	N	N	N	N	N	N	N	N	N
A41258	JH0557	S51959	S48992	S63131	S35049	S51892	T34513	T19474	I53641	F90073	T47182	S35047	A53715	T21460	S63257
		hypothetical prote	flocculation prote	probable membrane	mucin JER57 - huma	probable membrane	hypothetical prote	hypothetical prote	mucin 5AC - human	hypothetical prote	hypothetical prote	mucin JUL7 - human	apomucin precursor	hypothetical prote	probable membrane

ALIGNMENTS

Qy 297 N Db 639 1	Qy 237 7 Db 584 7	Qy 184 F Db 527 J	Qy 124 E Db 480 E	Qy 89 - Db 420 E	Qy 52 N Db 363 N	Query Match Best Local Si Matches 93;	RESULT 1 T29634 hypothetical protein C12D12 C;Species: Caenorhabditis e C;Date: 15-Oct-1999 #sequen. C;Accession: T29634 R;Nhan, M.; Hawkins, J. submitted to the EMBL Data A;Description: The sequence A;Reference number: Z20656 A;Accession: T29634 A;Status: preliminary; tran A;Molecule type: DNA A;Residues: 1-825 < NHA> A;Cross-references: EMBL:U5 A;Experimental source: stra C;Genetics: A;Amap position: X A;Introns: 48/1; 86/3; 137/ C;Superfamily: Epstein-Barr
MATPTDSKGSLETIPFT 323	TTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPITLISTVETRAAATLQA 296 :	KLFKMDEASAQLLAYKEKGHSQSSQFSSDQBIAHLLPENVSALPATVAVASPH 236 	PSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLE 183	TAROPNCYLFFCPNEEACPLKPAKGLMSYRIITDF 123	NEPVYTSTQEDCINSCCSTKNISGDKACNLMIFDTRK	/ Match 7.9%; Score 174.5; DB 2; Length 825; Local Similarity 23.7%; Pred. No. 0.00051; 1es 93; Conservative 40; Mismatches 144; Indels 115; Gaps 17;	RESULT 1 T29634 C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T29634 C;Accession: T29634 R;Nhan, M.; Hawkins, J. submitted to the EMBL Data Library, March 1996 A;Description: The sequence of C. elegans cosmid C12D12. A;Reference number: Z20656 A;Description: The sequence of C. elegans cosmid C12D12. A;Accession: T29634 A;Cross-references: EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP:C12D12.1 A;Experimental source: Strain Bristol N2; clone C12D12 C;Genetics: A;Genetics: A;Gene: CESP:C12D12.1 A;Map position: X A;Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1 C;Superfamily: Epstein-Barr virus membrane antigen gp350

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A; Molecule type: mRNA
A; Residues: 1-211,'S',213-224,'AR',227-259,'S',261-477 <POR>
A; Cross-references: EMBL: 334277; NID: 9563374; PIDN: CAA84031.1;
A; Experimental source: clone JER47
C; Genetics:
                                                                     hypothetical protein F56H9.1 - Caenorhabditis elegans () Species: Caenorhabditis elegans () Species: Caenorhabditis elegans () Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 () Accession: T22808 R; Burton, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:454136; OMIM:158373
A;Map position: 11p15.5-11p15.5
C;Keywords: glvcorretain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 08-Oct-1999
C;Accession: S53362; S71065
R;Guyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.I Biochem. J. 305, 211-219, 1995
Biochem. J. 305, 211-219, 1995
A;Title: Characterization of the human mucin gene MUC5AC: a consensus cystem A;Reference number: S53361; MUID:95126907; PMID:7826332
A;Accession: S53362
                  submitted to the EMBL Data A; Reference number: Z19618 A; Accession: T22808
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  A;Status:
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  preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHPEVSIEHLGQVVQCSREEGLVCRNQDQQGPFKMCLNYEVRVLCCETPKGCPVT---ST
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                                                                                                                                                                                                                                                                                                                                   TTSTTSAPTTSTTSTPQTSKTSAATSSTTSGSGTTPSPVTTTSTASVSKTSTSHVSVSKT
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                                                       Library, June 1996
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from
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  GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
              serine-rich protein - fission yeast (Schizosaccharomyces pombe) c;Species: Schizosaccharomyces pombe C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change C;Accession: T39903 #sequence_revision 03-Dec-1999 #text_change R;Lyne, M; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, November 1998 A;Reference number: Z21889
                                                                                                                                                         T39903
  A; Reference number: A; Accession: T39903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
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A; Accession: T22696
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A;Molecule type: DNA
A;Residues: 1-770 <WIL>
A;Cross-references: EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F56H9.1
A;Experimental source: clone F56H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z83318; PIDN:CAB05903.1; GSPDB:GN00022; CESP:F55B11. A;Experimental source: clone F55B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F55B11.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T22696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%;
Local Similarity 32.7%;
les 48; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                              49/3; 123/3; 226/1; 282/3; 669/3; 743/3
                                                                                                                                TVTSQPPTTLISTVFTRAAATLQAMA--TTAVLTTTFQAPTDS---KGSLETIPPTEIS- 326
                                                                                                                                                                                                                                                     LPENVSALPATVAVAS-----PHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVT 272
                                             ---NLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLP 380
                                                                                                                                                                                                     VPTTTTTVPTTTTTVSTTTTTVPTTTTVPTTTTVPTTTTVPTTTTVPTTTTSVPTTTTTVPTT 436
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PTTTTTVPTTTTTVPTTTTTVSTTTTTVPTTTTTVPTTTTTVSTTTTTVPTTTTVP
                                                                                                  TTTVPTTTTVSTTTTTVPTTTTTVSTTTTTVPTTTTVPTTTTTVPTTTTTVPTTTTTVPTTTTSV
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                                                                                                                                                                                                                                                                                                     Score 154.5; DB 2;
Pred. No. 0.012;
6; Mismatches 89;
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17-Nov-2000

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A;Status: preliminary; translated fr
A;Molecule type: DNA
A;Residues: 1-534 <LYN>
A;Cross-references: EMBL:AL033534; P
A;Experimental source: strain 972h-;
C;Genetics:
A;Gene: SPDB:SPBC215.13
A;Map position: 2
C;Superfamily: pig submaxillary muci
                                                                                                                                                                                                                                                                                 A;Residues: 1-1251 <WIL>
A;Residues: 1-1251 <WIL>
A;Cross-references: EMBL:Z47072; PIDN:CAA87369.1; GSPDB:GN00020; CESP:F26C11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F26C11.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21389
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                                                                                                                                            Query Match
Best Local S
Matches 93
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Best Local
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                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEYTPSSTESSSLLDPSS--VSSAILPSSTSVEVSISSSSLSSSDPLTSSTFSSLSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GNEPVY-----TSTQEDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCP-
                                                             CDCVLTSSSTETGTVKFLDREFFRVFSSAEIASTTSLPTTTSPSLNCYWLSEPSNFSEWI 141
                                                                                                    CFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCI-----
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                                                                                                                                            Conservative
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  --NSCCSTKNI----SGDKACNLMIFDTRKTARQPNCY--LFFC-PNEEACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%; Pred. No. ... ative 79; Mismatches 183;
                                                                                                                                                            6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Library,
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Pred.
                                                                                                                                            Score 151.5; DB Pred. No. 0.031; 6; Mismatches 1
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-; cosmid c215
                                                                                                                                                                                                                                                                                                                                                                                                                                            December
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No. 0.0071;
                                                                                                                                                                               DB 2;
                                                                                                                                            161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:92295566; PMID:1318606
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
C;Genetics:
C;Genetics:
A;Gene: 71
C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1
C;Superfamily: equine herpesvirus glycoprotein
F;1-22/Domain: signal sequence #status predicted <NAT>
F;23-797/Product: glycoprotein; X #status predicted <MAT>
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F;489-797/Domain: equine herpesvirus glycoprotein homology <EHG>
F;489-797/Domain: transmembrane #status predicted <TMN>
F;766-790/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M86664; NID:g330791; PIDN:AAB02506.1; PID:g330862 R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. Virology 189, 304-316, 1992
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A; Residues: 1-797 < TEL>
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Matches 58
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Similarity 24.3%;
SKGSLETIPFTEISNLTILNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGS
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                                                             LLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTP----------
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                                                                                                                                            SAPSTASSTTSIPTSTSTETTTTTPTASTTTPTTTTAAPTTAATTTAVTTAASTSAETTT 148
                                                                                                                                                                                                                      TTSSSSTSGSGQSTSSGTTNSSSSPTTSPPTTSSSPPTSTHTSSPSSTSTQSSSTAATSS
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                                                                                                ---SGTSQPQLAT-TAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTD
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                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                  Score 150.5; D
Pred. No. 0.02;
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N;Alternate names: mucin SMUC-41
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text change 05-Nov-1999
C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text change 05-Nov-1999
C;Accession: A49863; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963
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C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-22/Domain: signal sequence #status predicted <SIG>
F;22-39/Domain: catalytic #status predicted <CAT>
F;23-860/Product: chitinase 2 #status predicted <MAT>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Isolation and characterization of A; Reference number: JC4565; MUID: 96144270; A; Accession: JC4566
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A; Cross-references:
                       A; Molecule type: mRNA
A; Residues: 1-639 < GU1>
                                                                                                                                                                                                                                                                                                mucin 2 precursor, intestinal - human (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-860 < PIS>
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;687-860/Region: cysteine-rich
;90,657/Binding site: carbohydrate (As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: JC4566
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;Alternate names: chitin hydrolase homolog; CTS2 protein
;Species: Coccidioides immitis
;Cate: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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23.9%; Pred. No. 0.02
htive 49; Mismatches
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R;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner, Biochem. Blophys. Res. Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t A;Reference number: PQ0328; MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915
A;Residues: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864
A;Cross-references: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864
A;Note: sequence inconsistent with the nuclectide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
A;Che: Bequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
A;Che: Bequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
A;Che: Bequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
A;Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis
A;Reference number: A33532; MUID:89197956; PMID:2703501
A;Accession: B33532
A;Molecula type: mRNA
A;Residues: 1916-2193 <GU4>
A;Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874
A;Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874
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R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.
J. Clin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. 1
A;Reference number: A43932; MUID:91358717; PMID:1885763
A;Accession: A43932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; J. Clin. Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the same mucin A;Reference number: A61257; MUID:91086481; PMID:1985113
A;Accession: A61257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; J. Biol. Chem. 267, 21375-21383, 1992 A;Title: The human MUC2 intestinal mucin has cysteine-rich A;Reference number: A45106; MUID:93016075; PMID:1400449 A;Accession: A45106
                                                                                                                                                                                                          A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von C;Keywords: glycoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:MUC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 2328-2342, 'K', 2344-2354 < XUG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: P00329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: small intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 2328-2468 < XUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: bronchus
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A; Residues: 'T', 1925-1948, 'TTS', 1952-1954 <JAN>
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A; Residues: 2037-3020 <GU3>
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A; Residues: 626-1895
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                                                                     Matches
                                                                                                                                    Query Match
                                                                                                       Similarity
PENVSALPATVAVASPHTTSATPKPATL--LPTNASVTP--SGTSQPQLATTAPPVTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:M86523
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                                                                                                       6.8%;
34.1%;
                                                                     12;
                                                                                                       Score 149.5; D
Pred. No. 0.13;
                                                                                                                                        DB 2;
                                                                     52;
                                                                                                                                        Length
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PASTITLPPITTPSPPITTTTPPPTTTPSPPTTTPITPPTSTTTLPPTTTTPSPPPTTTT

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R;Miller, N. submitted to the EMBL Data Library, April A;Description: The sequence of C. elegans A;Reference number: Z21500
A;Accession: T34293
A;Accession: T34793
                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-790 < MIL>
                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_rev
C;Accession: T34293
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hypothetical protein F49E10.2 - Caenorhabditis elegans
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A;Title: Human mucin gene MUC5B, the 10.7 kb large central
A;Reference number: 222899; MUID:97166151; PMID:9013550
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                                                                                                                                                                  A;Cross-references: EMBL:U53341; PIDN:AAC69106.1; GSPDB:GN00028; CESP:F49E10.2
A;Experimental source: strain Bristol N2; clone F49E10
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A; Residues: 1-3570 < DES>
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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                                                                                          A;Introns: 51/1; 92/3; 176/3; 235/3; 332/2; 514/1; 543/2; 569/3; 677/1;
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Query Match
Best Local Similarity 25...
60; Conservative
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Matches
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                                    6.7%;
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                  Score 147.5; DB 2;
Pred. No. 0.032;
4; Mismatches 107;
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Pred. No. 0.16;
2; Mismatches
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cosmid
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                    107;
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                                                    Length
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                  33;
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A;Residues: 1-1609 <WIL>
A;Cross-references: GB:X59720; EMBL:S43845; NID:g1907116;
R;Frontali, L.; Grisanti, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable membrane protein YCR089w - yeast (Saccharomyces cerevisiae)

()Alternate names: hypothetical protein YCR1102

()Species: Saccharomyces cerevisiae

()Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 21-J

()Accession: S25345; S19504

R;Wilson, C.; Grisanti, P.; Frontali, L.

Yeast 8, 569-575, 1992

A;Title: The complete sequence of a 6146 bp fragment of Saccharomyce

A;Reference number: S25345; MUID:92397594; PMID:1523889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 3R
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: A;Map position: 3R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1609 <FRO>
A;Cross-references: EMBL:X59720; NID:g1907116; PID:e264634; PID:g1907227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S19504
A; Accession: S19504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: SGD:FIG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the Protein Sequence Database,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;1592-1609/Domain: transmembrane
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Best Local
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                  TTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPT--
                                                                                                                                                    SSDQEIAHLLPENVSALPATVAVASP------HTTSATPKPAT-----LLPTNASV
                                                                                                                                                                                                          KTVYTTWCPLTSKSTLGATTQTSSTAKVRITSASSATSTSISLSTSTESESSSGYLSKGV 1225
                                                                                                                                                                                                                                                                                       TTWCPLAEKSTV--AASSQSSRSVDRFVSSSK--PSSSLSQ--TSIQYTLSTATTTISGL 1165
                                                                                                                                                                                                                                                                                                                                                                                                     IQSSLSKGIRGNEPVYTSTQEDCINSCCSTKNISGDKACNLMIFDTR----KTARQPNCY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WQ----KVQTGQNTLPPLFPVSKRVEEKVEKVS----AKP-NESDNKIPEQK 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLAHHHTDYSKPTDISWRDTLSQKF--GSSDH--LEKLFKMDEASAQLLAYKEKGHSQSS
                                                      SASSPSSTSLLSTSLPSPAFTSSTLPTATAVSSSTFIASSLPLSSKSSLSLSPVSSSILM 1344
                                                                                                                                  CSGTECTQDVPTQ-SSSPASTLAYSPSVSTSSSSSFSTTTASTLTSTHTSVPLLPSSSSI
                                                                                                                                                                                                                                            HTDYSKPTDISWRDTLSQKFGSSDHLE-KLFKMDEASAQLLAYKEKGHSQSSQ-----F
                                                                                                                                                                                                                                                                                                                                                                 IMSSSSNVISTNEKPSSTTSPYNFSSGYSLPSSSTPSQYSLSTATTTINGIKTV----Y
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                                                                                          TPSGTSQPQLATT---APPVTTVTSQPPTTLISTVFTRAAATLQAMA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 147.5; I
Pred. No. 0.079
63; Mismatches
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RESULT 14
A47547
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A;Title: P-domains as shuffled cysteine-rich modules in A;Reference number: A45155; MUID:93077556; PMID:1447205 A;Accession: A45155
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A45155
A;Crose-references: FlyBase:FBgn0003319
C;Superfamily: serine proteinease stubble-stubbloid; trypsin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;61-77/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                              R;Appel, L.F.; Prout, M.; Abu-Shumays, R.; Hammonds, A.; Groc. Natl. Acad. Sci. U.S.A. 90, 4937-4941, 1993
A;Title: The Drosophila Stubble-stubbloid gene encodes an A;Reference number: A47547; MUID:93281671; PMID:7685111
A;Accession: A47547
                                                                                                                                                                                                                                             serine proteinease stubble-stubbloid (EC 3.4.21.-) - fruit fly (Drosophila C;Speciles: Drosophila melanogaster C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A47547
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C;Species: Xenopus laevis (African clav
C;Date: 26-May-1994 #sequence_revision
C;Accession: A45155
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                                                                                                A; Molecule type: mRNA
A; Residues: 1-786 < APP>
A; Cross-references: GB:
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A; Residues: 1-662 <HAU>
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                                                                  A; Gene: Sb-sbd
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Best Local S
Matches 49
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;573-613/Domain: trefoil
                                                                                   Genetics:
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                                                                                                GB:L11451; NID:g158511;
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1 homology <TRF4 >
1 homology <TRF5 >
1 homology <TRF5 >
1 homology <TRF6 >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 147; DB 2;
Pred. No. 0.028;
9; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g (fragment)
                                                                                                                                                                                                                                                                                             (EC 3.4.21.-) - fruit fly (Drosophila melanogaster)
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                                                                                                PIDN:AAA28918.1; PID:g158512
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                                                                                                                                                                                                                              Garbe, J.C.; Fristrom,
                                                                                                                                                                                              apparent
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C; Keywords: glycoprotein
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A; Map position: 11p15.5-11p15.5
                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: MUC6
                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: stomach A; Note: sequence extracted from
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-505 <TOR>
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N;Alternate names: MUC6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI backbone

    human
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R;Toribara, N.W.; Roberton, A.M.; Ho, S.B.; Kuo, W.L.; Gu J. Biol. Chem. 268, 5879-5885, 1993
A;Title: Human gastric mucin. Identification of a unique A;Reference number: A46629; MUID:93194895; PMID:7680650
A;Accession: B46629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B46629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:L07518; NID:g292045; PIDN:AAB61945.1; PID:g292046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 IITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTD------YSKPTDISW 168
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                                                                                                                                                                                                                                                                                                                                                                          89 TARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLH-GQFS 147
                                                                                                                                                                                                                                                            QA-VTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQS
                                                                                                                                                                                                                                                                                                                   SSRPPPPFTTHSPPTGSSPFS-STGPMT---ATSFKT-TTTYPTPSLPQTTPLTHVPPFS
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| VTPSGTSQPQLATTAPPVTTVT----SQPPTTLIS----TVF 287
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 144.5; DB 2;
Pred. No. 0.029;
37; Mismatches 101;
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Search Job ti	망	Ş	DЬ	ઠ્ઠ	В
Search completed: Job time : 24 secs	361	347	302	288	246
Search completed: April 28, 2004, 12:59:51 Job time : 24 secs	SASIHSTPTGTVP 373	347 ESSTMNKTASWEGREASPGSSSQGSVP 373	302 SPLSSTGPMTATSIKTTTTYPTPSHPQTTLTTHVPPFSTSSVTPSTHTVITPTHAQMST- 360	288 TRAAATLQAMATTAVLTTTFQAPTDSKGSLET-IPFTEISNLTLNTGNVYNPTALSMSNV 346	246 SHASSTHHPEVTPTSTTNVTPKSTSRDTSTPVTHTTSATSSRPPTPITTHSSPTRS 301

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<u>(4)</u>

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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유 성 유 성

197 163 Matches

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Conservative

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Mismatches

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Indels

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Gaps

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CFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCI------

CDCVLTSSSTETGTVKFLDREFFRVFSSABIASTTSLPTTTSPSLNCYMLSEPSNFSEMI 141
-----NSCCSTKNI----SGDKACNLMIFDTRKTAROPNCY--LFFC-PNEEACP 107

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151.5; DB 1 No. 0.024;	4 R I	It is prinformate te. The slong removed. nt (See ch).	/GenBank/DDBJ da (SCR) domain.	EMBL/GenBank/DDBJ d	da; Chromadorea; Rhabo Caenorhabditis.	ed) sequence update) annotation update) .3 in chromosome II.	1240 AA.	ALIGNMENTS	CANAL CHICK XENLA TICDI YEAST YEAST ZYEAST YEAST YEAST YEAST YEAST YEAST YEAST YEAST	
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P28968;
01-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Glycoprotein X precursor.
                                                                                                                                                                                                                                                                                   SEQUENCE
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SIGNAL
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PIR; H36802; VGBEX1
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MEDLINE=92295566; PubMed=1318606;
Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
"The DNA sequence of equine herpesvirus-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphanerpesvirinae; Varicellovirus.
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 ATATATSTPTTTTPTSTTTTTATTTVPTTASTTTDTTTAATTTAATTTAATTTAATTTAA
                                ---SGTSQPQLAT-TAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTEQAPTD
                                                                   SAPSTASSTTSIPTSTSTETTTTTPTASTTTPTTTTAAPTTAATTTAVTTAASTSAETTT
                                                                                                     LLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTP---
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25; Mismatches
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Matches 78
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SEQUENCE
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01-OCT-1996 (Rel. 34, Last
10-OCT-2003 (Rel. 42, Last
Endochitinase 2 precursor
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InterPro; IPR001579; Glyco_hydro_1 BAS.
Pfam; PF00704; Glyco_hydro_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
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nilarity 23.9%;
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Pred. No. 0.018;
9; Mismatches 1
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                                                       SKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGS
267
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MEDLINE=96144270; PubMed=8566773; Pishko E.J., Kirkland T.N., Cole G.T.; "Isolation and characterization of two chitinase-encoding (Cts1, Cts2) from the fungus Coccidioides immitis."; Eukaryota; Fungi; Ascomycota; Pezizomycotina; Evonygenales; mitosporic Onygenales; Coccidioides. NCBI_TaxID=199306; sequence update)
annotation update)
(EC 3.2.1.14). 860 ጅ Eurotiomycetes; genes ę glycosyl z

entities requires a license agreement (S or send an email to license@isb-sib.ch). use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/ restrictions EMBL a collaboration for តូ

Glycosidase; Chitin degradation; Chitin-binding; Signal; ENDOCHITINASE 2. N-LINKED (GLCNAC. . ; 5E34B54FAA663F3C POTENTIAL CRC64; (POTENTIAL)

DB 1;

Length

860;

밁 384 TVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFT TVSPSSTMQTTSTGSTSIETVTTRSQEPPSTTISTRSASTEPVTTRSQEPPSTTIS---LGGLPYADIMKEVILLRCDPDPPTSTVTSTTSASTSTQTSSQSTTMETKTLSASTTPSSPS TDFPSLTRNLPSQE--LPQEDSLLHGQFSQAV-TPLAHHTDYSKPTDISWRDTLSQ--NPSCSAKRWVTNPKSVTYTVDDWVKYIRKSGNPLAKLFI-NSCCSTKN-ISGDKACNLMIFDTRKTARQ---PNCYLFFCPNEEACPLKPAKGLMSYRII 120 FGSSDHL----EKLFKMD----EASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPA -GLPASKSAAAKEDYLTPGEATKIVSTYMAKYPSTFGGM--MVWEATASENNK 141; Indels 59; Gaps × 228 175 383 323 440 273

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CZ HUMAN STANDARD; PRT; 5179
CMUC2 HUMAN STANDARD; PRT; 5179
Q02817; Q14878;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence updat
28-FEB-2003 (Rel. 41, Last annotation upo
Mucin 2 precursor (Intestinal mucin 2).
MUC2 OR SMUC.
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and polymorphism.";
J. Clin. Invest. 88:1005-1013(1991).
J. FUNCTION: Coats the epithelia of the intestines, and investing organs. Thought to the companies of the intestines and investigation of the intestines, and investigation of the intestines of the intestines of the intestines.
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SEQUENCE OF 1343-1895 AND 4176-4195 FROM MEDLINE=91358717; PubMed=1885763; Toribara N.W., Gum J.R. Jr., Culhane P.J Petersen G.M., Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The
                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                              agents at mucosal surfaces.

-!- SUBURIT: Multimeric.
-!- SUBCELIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: COLON, SWALL INTESTINE, COLONIC TUMORS,
-!- TISSUE SPECIFICITY: COLON, SWALL INTESTINE, COLONIC TUMORS,
--- BRONCHUS, CERVIX AND GALL BLADDER.
-!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
--- POLYMORPHISM: The number of repeats is highly polymorphic and
varies among different allels.
--- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain
--- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
--- SIMILARITY: Contains 2 VWFC domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Intestine;
MEDLINB=94137002; PubMed=8300571;
MEDLINB=94137002; PubMed=8300571;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim "Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the amino terminus and overall sequence to prepro-von Willebrand factor.";
J. Biol. Chem. 269:2440-2446(1994).
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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MEDLINE=93016075; PubMed=1400449;
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Pfam; PF001826; TIL; 1.
Pfam; PF00093; vwc; 1.
Pfam; PF00094; vwd; 4.
SMART; SM00214; VWC; 2.
SMART; SM00216; VWD; 4.
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09HC84; 000447; 000573; 014985; 015494; 095291; 095451; Q14881.
099552; 09UE28;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Mucin 58 precursor (Mucin 5 subtype B, tracheobronchial) (High molecular weight sallvary mucin MG1) (Sublingual gland mucin).
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SEQUENCE OF 40-1324 FROM N.A. MEDLINE=99023932; PubMed=9804771; Desseyn J.-L., Butsine M.P., Porce "Genomic organization of the huma
                                                                                                                                                                                                              MEDLINE=99009274; PubMed=9790959; Offner G.D., Nunes D.P., Keates A.C., Af "The amino-terminal sequence of MUC5B comultifunctional D domains: implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-1594 FROM N.A.
Chen Y., Di Y.P., Wu R.,
"Molecular cloning of the amino-terminal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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Aubert J.-P., Laine A gene MUC5B: cDNA and
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"Human mucin gene MUCSB, the 10.7 kb lavarious alternate subdomains resulting evidence for a 11p15.5 gene family."; J. Biol. Chem. 272:3168-3178(1997).
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     EMBL;
EMBL;
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MEDLINE=97293229; PubMed=9164870;

MEDLINE=97293229; PubMed=9164870;

Keates A.C., Nunes D.P., Afdhal N.H., Troxler R.F., Offi

"Molecular cloning of a major human gall bladder mucin:

terminal sequence and genomic organization of MUC5B.";

Biochem. J. 324:295-303(1997).
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-i- FUNCTION: Salivary mucin that is thought to contribute to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97166151; PubMed=9013550; Desseyn J.-L., Guyonnet-Duperat V.,
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J. Biol. Chem. 273:30157-30164(1998).
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MEDLINE=96125355; PubMed=8554565;
MEDLINE=96125355; PubMed=8554565;
Troxler R.F., Offiner G.D., Zhang F., Iontcheva I., C
"Molecular cloning of a novel high molecular weight
from human sublingual gland.";
from human sublingual gland.";
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                                                                                                                                                                                                                                                                                                               Biol. Chem. 272:16873-16883 (1997).

FUNCTION: Salivary mucin that is thought to contribute to the lubricating and viscoelastic properties of whole saliva.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Expressed mainly in bronchus glands and also in submaxillary glands, endocervix, gall bladder, and pancreas.

PTM: Highly glycosylated.

PTM: Highly glycosylated.

SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.

SIMILARITY: Contains 3 VWFC domains.

SIMILARITY: Contains 4 VWFD domains.

SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
AF107890; AAG33673.1; -.
AF008604; AAC6755.1; -.
AJ004862; CAA06167.1; -.
Z72496; CAA96577.1; -.
Z72496; CAA52910.1; -.
Z04995; CAA52910.1; -.
Z04995; AAB61398.1; -.
Z049854; AAC51344.1; -.
Z049854; AAC51344.1; -.
Z049853; AAC51344.1; JOINED
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                                                                                                                                                                                     equires a license agreement (S email to license@isb-sib.ch).
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DR MIM; 600770; ...

RIM; 600700; ...

DR Incerpo; IRR006201; Cye knot. C.

DR Incerpo; IRR006201; Cye knot. C.

DR Incerpo; IRR006201; Cye knot. C.

DR Incerpo; IRR006201; MPG_CL,

DR Incerpo; IRR006201; MPG_CL,

DR Incerpo; IRR006201; MPG_CL,

DR Ffam; PP00091; VWG, 6.

DR Ffam;
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SEQUENCE OF 193-1 TISSUE-Lung, MEDLINE-94230376; Meerzaman D., Cha Martin B.M., Rose "Cloning and anal human tracheobron	Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606; [1] SEQUENCE OF 1-372 FR MEDLINE=21426417; Pu Escande F., Aubert J "Human mucin gene MU repetitive region."; Biochem. J. 358;763-	LT 6 A HUMAN MUSA, HUMAN P9808; O760 01-FEB-1996 28-FEB-2003 28-FEB-2003 MUCIN 5AC (M MUCIN 5AC (M MUCSAC OR MU HOMO SADIENS	349 2113	305 2054	263 1994	204 1951	Query Match Best Local S Matches 62	CONFLICT CONFLICT	CONFLICT CONFLICT	CONFLICT CONFLICT	CONFLICT	CONFLICT	CONFLICT	CARBOHYD
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FROM bMed=: s P., C.; C.; g of c	Metazoa; Chordata; Eutheria; Primates; =9606; F 1-372 FROM N.A. 426417; PubMed=1153 , Aubert JP., Por in gene MUCSAC: org region.";	ARD; 92; , Cr , La , La ubty	TMNKTASWEGREASPGSSSQGS : : GSMATPSSSTQTS	PTDSKGSLETIPF : : .TPSSSPGRARTLP-	STATP	DQEIAHLLPE	6.8%; y 30.5%; rvative	629 633 676	512 587 601	374 394 469	355 362 362	331 331	34	5662 5137
IN.A., AND PARTIAL SEQUENCE. 7513696; Daskal E., Polymeropoulos M.H., CDNA encoding a major airway glycoprotein, cin (MUC5).";	ofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Eutheria; Primates; Catarrhini; Hominidae; Homo. axID=9606; 2E OF 1-372 FROM N.A. 3=21426417; PubMed=11535137; 3 F., Aubert JP., Porchet N., Buisine M.P.; mucin gene MUC5AC: organization of its 5'-region and central cive region."; n. J. 358:763-772(2001).	PRT; 1233 AA. Q8WWQ3; eated) st sequence update) st annotation update) pe AC, tracheobronchial) ray glycoprotein) (Fragment).	SSQGS 371 : STQTS 2127	TIPFTEISNLTLNTGNVYNPTALSMSNVES 34	TSQPPTTLISTVFTRAAATLQAMATTAVLT 304 	QSSQFSSDQEIAHLLÞENVSALÞATVAVA-SPHTTSATÞKÞATLLÞTNASVTÞSGTSQÞ 262 :::	Score 149.5; DB 1; Length 5703; Pred. No. 0.22; 22; Mismatches 58; Indels 61; Gaps 10	DP -> RS (IN REF. 2). F -> L (IN REF. 2). A -> P (IN REF. 3).	-> P (IN REF. 2). A -> AH (IN REF. -> S (IN REF. 3).	> N (IN REF. 2). -> TR (IN REF. 2). -> GR (IN REF. 2).	41	(IN REF. (IN REF.	O14123. N REF. 2). LPCLCK (IN REF.	N-LINKED (GLCNAC) (POTENTIAL). T -> S (in dbSNP:2672788).

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REMBL; AJ298319; CAC83676.1; -.

REMBL; U06711; AAA18431.1; -.

REMBL; AJ001402; CAA04737.1; -.

REMBL; AJ001403; CAA04738.1; -.

REMBL; AJ001403; CAA04738.1; -.

REMBL; AJ001403; CAA04738.1; -.

REMBL; AJ001403; CAA04738.1; -.

REMBL; Z48314; CAA88307.1; -.

REMBL; AJ001403; CAA04738.1; -.

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J. Biol. Chem. 270:13665-13673(1995).
-i- FUNCTION: MAJOR AIRWAY GLYCOPROTEIN.
-i- SUBGLIGHT: Multimeric.
-i- SUBGLIGHT: TRACHEOBRONCHIAL MUCOSAE (NOT SOLELY).
-i- SUBGLIGHTY: TRACHEOBRONCHIAL MUCOSAE (NOT SOLELY).
-i- SIMILARITY: Contains 1 VMFD domain.
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Lesuffleur T., Roche F., Hill A.S.,
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P35653;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Factor induced gene 2,
FIG2 OR YCR089W OR YCR89W OR YCR1102.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
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                                          WIDLINE=92397594; PubMed=1523889; Wilson C., Grisanti P., Frontali L.; "The complete sequence of a 6146 bp fragment of cerevisiae chromosome III contains two new open Yeast 8:569-575(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
             -!- FUNCTION: Required for efficient -!- INDUCTION: By mating pheromones.
                                                                                                                          SEQUENCE FROM N.A.
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46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               PTTSTTSAPTTSTTSGPGTTPSPVPTTSTTSAP
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G -> A (IN REF. 3).

H -> Q (IN REF. 3).

A -> R (IN REF. 2).

A -> R (IN REF. 2).

R -> P (IN REF. 4).

S -> T (IN REF. 2).

G -> R (IN REF. 2).

A -> R (IN REF. 2).

A -> R (IN REF. 2).

G -> R (IN REF. 2).

CRSPUSDIARAPOTSSTLAS (IN REF. 2).

CRSPUSDIARAPOTSSTLAS (IN REF. 2).
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Pred. No. 0.038;
0; Mismatches
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SPR -> RPP (IN REF. 2).
G -> A (IN REF. 2).
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GTCAPVQAAAALNTLSTPAFLWRVWAMGHLLPGGGALTHPA
CSHLSGPAPGLAELLWPCIQPAVLGT (IN REF. 4).
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GRALLPEVHHPGVPPGPRGADPQASPRGVDKRDHLQQQGGQ
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VYGHFRVLVDNYFCGAEDGLSCPRSIILEYHQDRVVLTRKP
VHGVWTNEIIFNNKVVSPGFR -> ITTSASVCAAAGVTPT
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NI)
                             mating
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373

Saccharomyces reading frame

frames.";

REF. 3).

RRSAVAPV

RTCAHHLPSRQGVPALR

DB 1; 80;

Length Indels

7;

Gaps

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67

341 127

CRC64;

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Query Match
Best Local S
Matches 88
                                                                                                                                                                                                                             MUC1_XE
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J. Biol. Chem.
                                                                                    SEQUENCE FRO
TISSUE=Skin;
                                                                                                                              01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Integumentary mucin C.1 (FIM-C.1) (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                      XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S25345; S25345.
GermOnline; 138986; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                                   "P-domains as shuffled cysteine-rich C.1 (FIM-C.1) from Xenopus laevis. Po
                                                            Hauser F., Hoffmann
                                                                      MEDLINE=93077556; PubMed=1447205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; S0000685; FIG2.
GC:0009277; C:cell wall (sensu Fungi); IDA.
GC:000075; P:cellular morphogenesis during conjugation
GC:0000755; P:cytogamy; IMP.
UENCE 1609 AA; 166049 MW; 7D66AD7F85A7B852 CRC64;
Niol. Chem. 267:24620-24624(1992).
FUNCTION: Could be involved in defense against microbial
                                                                                                                                                                                                                                                                                                    1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTWCPLAEKSTV--AASSQSSRSVDRFVSSSK--PSSSLSQ--TSIQYTLSTATTTISGL 1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMSSSSNVISTNEKPSSTTSPYNFSSGYSLPSSSTPSQYSLSTATTTINGIKTV-----Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000519; P_trefoil.
Pfam; PF00088; trefoil; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L02115; AAA74725.1;
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01359; 2PSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections. Protects the epithelia from extern SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist. 1
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SIMILARITY: Contains 6 P-type (trefoil) domains.
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SSUE SPECIFICITY: Skin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q05049-5; Sequence=VSP_004646, VSP_004649,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q05049-4; Sequence=VSP_004647,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q05049-1;
                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                       PR00680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content is in and this statement is not removed. Usage by and for corrections
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                                                                                                                                                                                                                                        P-TYPE
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                                                                                               APPROXIMATE
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STUB_DROME
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Matches 49
 STUB_DROME STAN
Q05319;
Q05319;
Q1-JUN-1994 (Rel. 2
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SB OR SB-SBD.
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          29, Last sequence update)
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MEDLINE=93281671;
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CRC64;

POLY-THR.

POLY-SER.

POLY-SER.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .)

Transmembrane; Glycoprotein;

Zymogen;

NON-CATALYTIC CHAIN (POTENTIAL).
CATALYTIC CHAIN (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).

SER/THR-RICH

POLY-GLN.

SERINE PROTEASE

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MEROPS; S01.225; -.
FlyBase; FBgn003319; Sb.
GO; GO:0004252; F:serine-type endopeptidase act
GO; GO:0007010; P:cytoskeleton organization and
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Ffam; PF00089; trypsin; 1.
R PFIAM; PF00089; trypsin; 1.
R PRINTS; PR00722; CHYMOTRYPSIN.
R SMART; SM00020; Tryp_SPC; 1.
JR PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
DR PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L11451; AAA28918.1; -. PIR; A47547; A47547. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane serine protease morphogenesis.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appel L.F., Prout M., Fristrom D., Fristrom
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fristrom D., Fristrom J.;
"The Drosophila Stubble-stubbloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Hormone dependent protease required for epithelial morphogenesis. Has a dual function, detaches imaginal disc of from extracellular matrices through its extracellular proteol domain and transmits an outside-to-inside signal to its intracellular domain to modify the cytoskeleton during morphogenesis. May be able to activate itself. SUBCELLULAR LOCATION: Type II membrane protein. INDUCTION: No Yorkelver and the cytoskeleton during in the cytoskeleton during morphogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDUCTION: By 20-hydroxyecdysone (20HE).
SIMILARITY: Belongs to peptidase family S1.
CAUTION: It is uncertain whether Met-1 or Met-24 is the initiator.
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                       Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                           SGD; S0004936; YMR317W.
Hypothetical protein; Repeat.
SEQUENCE 1140 AA; 113070 MW;
                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288c / AB972;
MEDLINE=97313268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 113.1 kDa protein in PRE5-FET4
YMR317W OR YM9924.09.
                                                                                                                                                                EMBL; 254141; CAA90835.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                              GermOnline;
                                                                                                                                                                                                                                                                                                                                                                                       Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
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      63;
                      Score 144.5; DB Pred. No. 0.063;
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                  EMBL; U14133; AAA69538.1; PIR; S53871; S53871. MGD; MGI:98301; Si.
                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6; TISSUE=Skin;
MEDLINE=95175358; PubMed=7870580;
Kwon B.S., Halaban R., Ponnazhagan S.,
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                                                                                                                    entities requires
                                                                                                                                         modified
                                                                                                                                                                                                                                                                                                                                                                                                                       putative cytoplasmic domain of Pmel Nucleic Acids Res. 23:154-158(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Melanocyte protein Pmel 17 precursor (Silver
SILV OR PMEL17 OR D10H12S53E OR SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mouse silver mutation is caused by a single butative cytoplasmic domain of Pmel 17.";
                         s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and for ifield the statement is not removed.
                                                                                                                                                                                                                                                                                                    FUNCTION: Could be a melanogenic enzyme.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: Preferentially expressed in melanocytes.
DISBASE: DEFECTS IN SILV ARE THE CAUSE OF THE SILVER COAT COLOR
WHICH SEEMS TO BE DUE TO PREMATURE DEATH OF PIGMENT CELLS DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQ-------
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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RESULT 12
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SM00089; PKD; 1.
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94; Conservative
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                                                                                                                                                                   QVVLQAAIPLVSCGSSPVPGTTDGYMPTAEAPGTTSRQGTTTKVVGTTPGQMPTTQPSGT
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                                                                                                                                                                                                      TKHFLRNHPLIFALQLHDPSGYLAEADLSYTWDFGDGTGTLISRALDVTHTYLESGSVTA
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                                                                                               GT--TPTRPSGTTVAQAT----TTEGPDASPLLPTQSSTGSI
                                                                                                                GNVYNPTALSMSNVESSTMNKTASWEGREAS---PGSSSQGSV 372
                                                                                                                                                   TVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNT
(Fragment)
                                                                                                                                 TVVQMPTTEVTAT----TSEQMLTSAVIDTT---
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                                                    STANDARD;
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     sequence update)
annotation update)
(Retinal pigment epithelial-specific
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N-LINKED (GLCNAC...) (POTEN)
N-LINKED (GLCNAC...) (POTEN)
N-LINKED (GLCNAC...) (POTEN)
S -> L (IN SILVER).
R -> G (IN SILVER).
D -> N (IN SILVER).
F -> S (IN SILVER).
AAPASGLARAGLGENSPLLSGQQV -> SS
RKQPAPQWTAGLIILKAFWISWG (IN SI
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Pred. No. 0.037
52; Mismatches
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MELANOCYTE PRO
EXTRACELLULAR
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7 X 13 AA APPROXIMATE TANDEM
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CYTOPLASMIC (POTENTIAL)
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SILVER).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The CDNA RPE1 and monoclonal antibody HMB-50 define gene preferentially expressed in retinal pigment epithelium."; Exp. Eye Res. 55:657-662 (1992).
-I- FUNCTION: Could be a melanogenic enzyme (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; NCBI_TaxID=9913; [1]
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Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M81193; AAA30419.1; -. PIR; A49179; A49179.
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-!- TISSUE SPECIFICITY: Retinal pigment epithelium.
-!- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.
-!- SIMILARITY: Contains 1 PKD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Retina;
MEDLINE=93122163;_PubMed=1478275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000601; PKD.
            178
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
TTPGQVPTAEAPGTTVGWVPTTEDVGT
                                                                                                                                                                                                                                                 RDTLSQ------KFGSSDHLEKLFKMDEASAQL----LAYK-EKGHSQSSQFSSDQE
                                                                                                                                                                                                                                                                                             PVSGL---SIGTDKAMLGTYNM-----EVTVYHRRGSQSYVPLAHSSSAFTITDQVPF
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                                                        TSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTT-FQAPT-DSKGS
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                                                                                                    VTHTYLESGPVTAQVVLQAAIPLTSCGSSPVPGTTDRHVTTA-EAPGTTAGQVPTTEVMG
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N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                            Score 142.5; D. Pred. No. 0.03;
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-LINKED (GLCNAC. . .) (PI
2BBFE5DFBD397D6D CRC64;
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              TPEQVATSKVLSTTPVEMPTAKATGR
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use by non-profit institutions as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                       SIGNAL
                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Binds to P-, E- and L-selectins. The calcium-dependent high affinity interaction with selectin mediates the tethering and rolling of neutrophils and T-lymphocytes on endothelial cells SUBUNIT: Homodimer; disulfide-linked (By similarity). SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                        adhesion;
                                                                                                                                                                                                                    MGI:106689
                                                                                                                                                                                                                                                                                                                                 P-selectin binding (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                   87:4176-4186(1996).
                                                                                                                                                                                                                                                                                                                                          Highly O-glycosylated. Also N-glycosylated (By similarity) Sulfated in the N-terminal region; sulfation is necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPEVSTTEPSGTTVTQGTTPELVETTAGEVSTPEPAGSN-TSSFMPTEGTAGSLS--PLP
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
 Glycoprotein;
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 Chordata;
Rodentia;
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                                                                              SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POT
N-LINKED (GLCNAC. . .)
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P-SELECTIN GLYCOPROTEIN LIGAND EXTRACELLULAR (POTENTIAL).

POTENTIAL.
                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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RESULT 14
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Best Local :
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DAN4 YEAST
P47179;
          entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                             Cohen B.D., Sertil O., Abramova N.E., Davies K.J., Lowry "Induction and repression of DAN1 and the family of anae mannoprotein genes in Saccharomyces cerevisiae occurs the complex array of regulatory sites.";
Nucleic Acids Res. 29:799-808(2001).
-!- FUNCTION: Component of the cell wall (By similarity) of DECELULAR LOCATION: Attached to the membrane by a content of the cell wall (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell wall protein DAN4 pr
DAN4 OR YJR151C OR J2223.
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10-OCT-2003 (Rel.
                                                                                             This SWISS-PROT entry is copyright. It is produced through a detween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                  MEDLINE=21113168; PubMed=11160904;
                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                 REGULATION
                                                  European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content titled and this statement is not removed. Usage by an
                                                                                                                                       PTM: Extensively O-glycosylated (Potential). SIMILARITY: Belongs to the SRP1 / TIP1 family.
                                                                                                                                                                 (Potential)
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Z49651; CAA89684.1;
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erevisiae occurs through
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RESULT 15

WSC2 YEAST STANDARD; PRT; 503 AA.

ID WSC2 YEAST STANDARD; PRT; 503 AA.

AC P53832;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell wall integrity and stress response component 2 precursor.

GR WSC2 OR YNL283C OR NO583
OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Agcomycota; Saccharomycotina; Saccharomycete
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Best Local Similarity
EMBL; 271559; CAA96195.1; -
PIR; S63257; S63257.
GermOnline; 143289; -.
SGD; S0005227; WSC2.
GO; GO:0005737; C:cytoplasm
GO; GO:0007047; P:cell wall
GO; GO:0007047; P:cell wall
GO; GO:0007046; P:response
GO; GO:00070266; P:Rho prote
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GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
InterPro; IPR000992; SRP1_TIP1.
Pfam; PF00660; SRP1_TIP1; 1.
PROSITE; PS00724; SRP1_TIP1; 1.
CREAK AND THE CONTROL OF THE CONTROL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Messenguy F., Dubois E., Vierendeels F., Scherens B., Pi
Glansdorff N.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales;
NCBI_TaxID=4932;
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  ; S0005227; WSC2.
G0:0005737; C:cytoplasm; IDA.
G0:0004888; F:transmembrane receptor activity; IGI.
G0:0007047; P:cell wall organization and biogenesis;
G0:0007047; P:response to heat; IGI.
G0:0007266; P:Rho protein signal transduction; IGI.
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REMOVED IN MATURE FORM (POTENTIAL)
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W; 7954C15D69F0CA58 CRC64;
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Mismatches
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Pfam; PF01822; WSC; 1.
SMART; SM00321; WSC; 1.
Cell wall; Transmembrane;
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SEQUENCE
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                                                 KWLLIGSLLFGVLFLVIGLVLL
                                                                           TSIGTSTHYTTRVVTQSVVSQANQQASTIFTTRTSVYATVSSTSSSTSSLLNGKSSSSKS 315
                                                                                               TEISULTLUTGUVYUPTALSMSUVESSTMUKTASWEGREASPGSSSQGSVPENQYGLPFE
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CELL WALL INTEGRITY A
COMPONENT 2.

POTENTIAL.
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Pred. No. 0.082;
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(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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      SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_blant:*
10: sp_blant:*
11: sp_vertebrate:
13: sp_vertebrate:
14: sp_unclassifie
15: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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2211
1 MFFGGEGSLTYTLVIICFLT.....LRRKRYSRLDYLINGIYVDI 431
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sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vertebrate:*
sp_unclassified:*
sp_trus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                  sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	· ហ	.4	ω	N	ш	Result No.
156.5	157.5	160.5	168	180.5	188	196.5	197	197.5	503	1164.5	1179.5	2022	2039	2210	2211	Score
7.1	7.1	7.3	7.6	8.2	8.5	8.9	8.9	8.9	22.7	52.7	53.3	91.5	92.2	100.0	100.0	Query Match 1
328	2448	477	519	1349	449	392	449	392	194	414	414	397	431	431	431	Query Match Length DB
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000446	Q8WWQ5	Q14887	Q7YTR7	Q8WWQ4	Q96F05	Q9D8N1	Q9H2K4	Q8VCP2	Q8K0I0	Q9CR33	Q80V71	Q9NW60	Q95KG7	Q8NEC1	Q9Н8J5	ID
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45	44	43	42	41	40	39	38	37	36	35	ω 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
141	141	141.5	142	142	142.5	142.5	142.5	142.5	142.5	143.5	143.5	144	144.5	144.5	144.5	144.5	145	145.5	145.5	146	146	147.5	147.5	150.5	152	154	155.5	155.5
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RESULT 2
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AC QBNEC1;
DT 01-OCT-2002 (
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DE Hypothetical
OS Homo sapiens
OC Eukaryota; Me
OC Mammalia; Eut
OX NCBI_TaxID=96
RN [1]
OS SEQUENCE FROM
RC TISSUE=Testis
RA Strausberg R.
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DR EMBL; BC03299
KW Hypothetical
SQ SEQUENCE 43
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC032998; AAH32998.1; -.
Hypothetical protein.
SEQUENCE 431 AA; 46824 MW; 1BCEEBD168AC835
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ10298.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-CCT-2003 (TrEMBLrel. 25, L
Hypothetical protein.
Macaca fascicularis (Crrab eat
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-Temporal cortex;
Osada N., Hida M., Kusuda J., Tanuma R
Suzuki Y., Sugano S., Hashimoto K.;
Suzuki Y., Sugano full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; AB060888; BAB46892.1; -. Hypothetical protein. SEQUENCE 431 AA; 47104 MW; BF10996E87F76C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae;
NCBI_TaxID=9541;
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Pred. No. 8.1e-146;
9; Mismatches 24;
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Q80V71;
Q1-JUN-2003 (TrEMBLrel. 2
Q1-JUN-2003 (TrEMBLrel. 2
Q1-JUN-2003 (TrEMBLrel. 2
Q1-JUN-2003 (TrEMBLrel. 2
Q130403P13R1k protein.
Mus musculus (Mouse).
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Q9NW60;
01-OCT-2000
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ10298.
Hymon sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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397 AA; 4
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92.1%;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschanko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robesk S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Wadan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Kraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Arnes S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,00
"Generation and equences.";
and mouse CDNA sequences.";
arad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-200;
EMBL; BC039930; AAI
SEQUENCE 414 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Breast tumor;
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EDCVGACCSTKDIAGDKACNIMIFDTRKTDRQPNCYLFFCPSEDACPLKPAKGIVTYRLI
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                                                               DYLINGIYVDI
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                                                                                                                                                                              EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
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AA; 44531 MW; 84AFB759D1B22755 CRC64;
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AC Q9CR3
AC Q9CR3
AC MARAN-2003
AC MAMMARIA EU
OX MCBI TAXADB EU
OX MCBI TAXADB EU
OX MCBI TAXADB EU
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,
A Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl R., Stabli F., Suzuki R., Tomita M., Magner L., Washio T.,
A Schriml L.M., Stabli F., Suzuki R., Tomita M., Barahio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Hayashtaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phy
"Analysis of the mouse transcriptome based on 1
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AKO18636; BAB31129.1; -.
EMBL; AKO18636; BAB31139.1; -.
EMBL; AKO18635; BAB31319.1; -.
EMBL; AKO18535; BAB31319.1; -.
EMBL; AKO18535; BAB23819.1; -.
EMBL; AKO46837; BAC28357.1; -.
EMBL; AKO46837; BAC2892.1; -.
EMBL; AKO46837; BAC2892.1; -.
EMBL; AKO46837; BAC3892.1; -.
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STRAIN-C57BL/6J; TISSUE-Colon, and Medulla
MEDLINE-22354683; PubMed-12466851;
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STRAIN=C57BL/6J; TISSUE=Cecum;
MEDLINE=21085660; PubMed=11217851;
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Hayashizaki Y.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
9130403P13Rik protein (Weakly similar to NT2RM1001115 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
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                                                         HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQETAHLLPENVSALPATVAVASPHTTSA
                                                                                                                            RDFPLTSANSSLQQLTQGEFLLLDHSSPGATPGFRTPAGYPKPTGLSWSDRSSLKSTAPL
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HLRKHIKADETSMQL---PEEKSHSQSLQLPSELKMAHLLPKTVPTPPTTVAVAPLRNVSA
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Matches 122
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Q8VCP2;
Q8VCP2;
Q1-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, I
01-OCT-2002 (TrEMBLrel. 22, I
RIKEN CDNA 1810055G02 gene.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to hypothetical protein FLJ10298 (Fragment)
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                          1810055G02RIK.
Mus musculus (Mouse).
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SEQUENCE 194 AA; 2
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation updat
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Pred. No. 3.1e-30;
                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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01-MAR-2001
01-OCT-2003
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Q9H2K4;
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SEQUENCE FROM N.A.
TISSUB-Liver;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019471; AAH19471.1; -.
MGD; MGI:1919306; 1810055G0ZRİK.
SEQUENCE 392 AA; 41081 MW; 1D79796C791211FA CRC64;
                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=21295044; PubMed=11401438;
Twells R.C.J., Metzker M.L., Brown S.D., Cox R., Garey C., Hammond H.
Hey P.J., Levy E., Nakagawa Y., Philips M.S., Todd J.A., Hess J.F.;
"The Sequence and Gene Characterization of a 400-kb Candidate Region
                                                                                                                                  for IDDM4 on Chromosome 11q13.";
Genomics 72:231-242(2001).

EMBL; APG44781; AAG36936.1; -.

InterPro; IPR001395; Aldo/ket_red.

PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.

SEQUENCE 449 AA; 46100 MW; 11C8B0FCC3BBF921 CRC64;
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human),
Eukaryota; Metazoa; (
Mammalia; Eutheria; E
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                                                     LVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCINSCCSTKN
ISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPS 132
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ilarity 22.2%;
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                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
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26.5%; Pro
ative 37;
                                                                                                                                                                                                                                                                                                                                                                                         16,
16,
25,
                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                              Score 197; DB 4;
Pred. No. 1.2e-06;
19; Mismatches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 197.5; DB 11
Pred. No. 9.3e-07;
7; Mismatches 115;
                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                449
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                                                                                                        Length 449;
                                                                               Indels 196;
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	Db Qy Db RESULT 1 Q9D8N1 ID Q9D AC Q9D DT Q1- DT 01- DT 01- DT 01- DT 181 GN 181 GN 181 GN 181 GN Mus OC Mam ON (101)	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=2108566J; PubMed=11217851; Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh.M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., "Functional annotation of a full-length mouse cDNA collection."; EMBL; AK007868; BAB25319.1; MGD; MGI:191306; 1810055GOZRik. SEQUENCE 392 AA; 41095 MW; 6BBA958C73489874 CRC64;	339 GTSQAPEQVETEATPGTDSTGPTPRSSGGTKWPATDSCQPSTQGQYMVVTTEPLTQAVVD 398 383 KWILIGSILFGVLFUVIGLVLLGRILSESLRRKRYSRLDVLINGIYVD 430	

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Q96F02
ID Q96F0
AC Q96F0
AC Q96F0
DT 01-D0
DT 01-D0
DT Chrom
OS Homo
OC Eukar
OC Mamma
OX NCEL
RN [1]
RN [1]
RN [1]
RN SEQUE
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Best Local Similarity
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Q96F05;
Q96F05;
Q96F05;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chromosome 11 open reading frame 24.
Homo sapiens (Human).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                   Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011765; AAH11765.1; -
Genew; HGNC:1174; Cliorf24.
InterPro; IPR001395; Aldo/ket_red.
PROSITE; PS00063; ALDOKETO_REDUCTASE 3; 1.
SEQUENCE 449 AA; 46142 MW; BF984ĀA360F6C415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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    248
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                                       STTAA-----SITTAASSMTVASSAP-TTAASSTTVASIAPTTAASSMTAASSTPMTL
                                                                      AQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHT-----TSATPKPATL
                                                                                                                          MEVITEDI ---
                                                                                                                                                         QELPQEDSLLHGQFSQAVTFLAHHHTDYSKFTDISWRDTLSQKFGSSDHLEKLFKMDEAS
                                                                                                                                                                                                -----PVTLTKG-----TSAAHLNS
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  ---LPTNASV--TPS--GTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT
                                                                                                                                                                                                                                                                               LVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDVTMAAAS---
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                              8.5%; Score 188; DB 4; 22.0%; Pred. No. 5.8e-06;
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                                                                                                                   ----SRTDVSEP-----ATSGVAADGVTSIAPTAVAS
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01-OCT-2003 (TrEMBLrel.
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repetitive region.";
Biochem. J. 358:763-772(2001).
EMBL; AJ298318; CAC83675.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=21426417; PubMed=11535137;

Escande F., Aubert J.P., Porchet N., Buisine M.P.;

"Human mucin gene MUC5AC: organization of its 5'-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GGEGSLTYTLVI----ICFLTLRLSASQNCLKKSLEDVVID-----IQSSLSKGIRGNE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 8.2%; Score 180.5; DB 4; Similarity 21.6%; Pred. No. 9.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                      -----VCRNQDQQGPFKMC--LNYEVR-----VLCCETPKGCPVTSTS 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVYTSTQEDCINSCCSTKNISGD-KACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPEPAPTPTV--VTTTKAQAREPTASPVPVPHTSPIPEMEAMSPTTQPSPMPYTQRAAGP 338
APTTSTTSTPQTSTISSPTTSTTPTPQTSTTSSPTTSTTSAPTTSTTSAPTTSTTSTPQT
                                                PPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNL
                                                                                                      STISA-PTTSTISAPTTSTTSAPTASTTSAPTSTSSAPTTNTTSAPTTSTTSAPITSTIS
                                                                                                                                                       ENVSALPATVAVASP--HTTSATPKPATLLPTNASVTP-----SGTSQPQLATTA 268
                                                                                                                                                                                                           APTTSTTSAPTTS------TTSAPTTSTTSTPQTTTSSAPTSSTTSAPTT 710
                                                                                                                                                                                                                                                           SKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLP
                                                                                                                                                                                                                                                                                                                                                                  GLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQ-----AVTPLAHHHTDY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGDKE-TYNNI IRSGEKI CRRPQEITRLQ-CRAKSHPEVSIEHLGQVVQCSREEGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQPSTQGQYMVVTTEPLTQAVVD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLETIPFTEISNLTLNTGNVYNPTAL-----SMS-NVESSTMNKTASWEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTSSPMSTRPSPSKHMPSDTAASPVPPMRPQAQGPISQVSVDQPVVNTTNKSTPMPSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A------VLTTTFQAPTDSKG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1349 AA; 135600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4DC3C1544F1E5EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
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Indels Length

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Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                         Q14887; PRELIMINARY;
Q14887;
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-JUN-2003 (TrEMBLrel. 2
   SEQUENCE FROM N.A.
TISSUE=Tracheobronchial mucosa;
Guyonnet-Duperat V., Audie J.,
                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mortimore B.J.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81044; CAE17706.1; -.
Hypothetical protein.
SEQUENCE 519 AA; 56012 MW; 93C2CFF9EC339D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7YTR7;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein C30H6.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7YTR7
                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                             Mucin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans: A platform investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVAVASPHTTSATEKPATLLETNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDLTSILFNALGTVTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----STMNKTASWEGREASPGSSSQGSVPEN----QYGLPFE---KWLLIGSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVPTTTTTTTTTTTTTTTTTTTTTTTTTTPAT----TTSVGNNYNDANYYNSNHNE
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%;
27.1%;
      Audie J., Debailleul V.,
                                                                                                                                                                                                                                                                                                            01,
01,
24,
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25, Last sequence up
25, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 168;
Pred. No. 0.
                                                                                                                                                           Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LMRKIFCNIQY
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                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350
                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96;
      Laine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
   A., Buisine
                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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      3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
Q8WWQ5
ID Q8WWQ
      SQUERRA PROPERTIES OF A REPORT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
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Best Local Similarity 24.4%;
Matches 66; Conservative 43
                                                                                                                                                                                                    Genew; HGNC:7515; MUCSAC.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005840; C:ribosome; IEA.

GO; GO:0005343; F:structural constituent of

GO; GO:000412; P:protein biosynthesis; IEA

InterPro; IPR001209; Ribosomal S14.

InterPro; IPR001209; RID:

InterPro; IPR001007; VWF_C.

InterPro; IPR001007; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBWWQ5

OBWWQ5;

O1-MAR-2002 (TrEMBLrel. 2

O1-MAR-2002 (TrEMBLrel. 2

O1-OCT-2003 (TrEMBLrel. 2
                                                                                     InterPro; IPR001007; VWF
InterPro; IPR001846; VWF
Pfam; PF01826; TIL; 2.
Pfam; PF00094; Vwd; 3.
SMART; SM00214; VWC; 3.
SMART; SM00216; VWD; 3.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repetitive region.";
Biochem. J. 358:763-772(2001).
EMBL; AJ298317; CAC83674.1; -.
PROSITE; PS00527; RIBOSOMAL_S14;
NON_TER 2448 2448
SEQUENCE 2448 AA; 260970 MW;
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Biochem. J. 0:0-0(1994).
EMBL; Z34277; CAA84031.1; -.
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Mammalia; Eutheria;
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"Human mucin gene MUC5AC:
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477 AA;
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Last annotation updat
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                                                                                                                                                2137 GGDKETYNNIIRSG---EKICRRPEEITRLQC-RAKSHPEVSIEHLGQVVQCSREEGLVC 2192
                                                                          2356 TTSASPAGTTSGPGNT 2371
                                                                                                                                                                                                                        2250 SRITTLVTTSTTSTPQTSTTYAHTTSTTSAPTARTTSAPTTSTTSVPTTSTISGPKTTPS 2309
                                                                                                                                                                                                                                                                                                 2193 RNQDQQGFKMCLNIEVRVLCCETPKGCPVT---STPVTAPSTPSGRAISPTQSTSSWQK 2249
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                                                                                                                                                                                                                                                                                                                                                                                                            169 ---RDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSS------QFSSDQ---- 213
                                                                                                         352 NKTASWEGREASPGSS 367
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